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RESULT 4
AAW97408
ID AAW9
XX AAW9
XX AAW9
AC AAW9
XX Lytl
XX magg
KW magg
KW magg
KW magg
XX Synt
XX Synt
XX W99
I1-1
XX W99
XX W99
I Van
XX WPI
PR 31-1
XX WPI
PR W1t
PR W1t
PF Con
DR W-P
XX IN-P
XX
RESULT 5
AAW99125
ID AAW9
XX
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                                                                                                                                                                                                                      Query Match

Best Local Similarity

Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents an lytic peptide which is used in the course of the inventin to produce transgenic poinsettia plants with increased resistance to pathogens. The specification describes methods for the in vitro regeneration of Poinsettia. Transgenic Poinsettia can now be produced with e.g. increased resistance to pathogens or insects; controllable flower colour; modified habit (more compact form, earlier
                  AAW99125 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              In vitro regeneration of Poinsettia - us containing casein hydrolysate, used to pu with, e.g. increased disease resistance, altered habit and flowering time
                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 51; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX16060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-153796/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    magainin; transgenic;
resistance; ethylene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lytic peptide magainin 2*S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW97408 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                         flowering)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SANF-) SANFORD SCI INC.
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                                                                                                                                16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                MGIGKFLHSAKKF 28
                                                                                                                                                                            IGIGKFLHSAKKF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KWKLFKKIGIGAVLKVLK 18
                                                                                                                                                                                                                                                                                                                                                         and/or
                                                                                                                                                                                                                                                                                                               39
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                                                                                                                                                                                                                                                                                                               A
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                                                                                                                                                                                                                                                                                                                                                            increased
                  peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein; 39
                                                                                                                                                                                                                                           59.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.3%;
72.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  poinsettia; in vitro regeneration;
flower colour.
                     39
                                                                                                                                                                                                                                                                                                                                                         resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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Pred. No.
                                                                                                                                                                                                                                           Score 64; DB 20; Pred. No. 0.0071;
                  A
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                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     using embryo-induction medium produce transgenic plants e, controllable flower colour,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
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                                                                                                                                                                                                                                                                                                                                                       ethylene.
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                                                                                                                                                                                                                                                            Length 39;
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                                                                                                                                                                                                                    Indels
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RESULT 6
AAY67472
ID AAY6
XX AAY6
XX AAY6
XX 12-A
DT 12-A
XX Maga
XX Ant:
KW Ant:
KW fun;
XX OS Un1.
XX
PN CA2
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                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents an antimicrobial peptide. The present invention also describes a method of conferring microbial resistance on a plant cell comprising transforming the cell to express two peptides selected from the magainin and PGL classes, where the peptides are separately compartmentalised. The antimicrobial peptide is effective against phytopathogenic microbes including bacteria, fungi, and phytoplasma. It can also be used to target other plant pests, such as nematodes and viruses. The nucleic acid sequence encoding the peptide can be used to transform plants to provide antimicrobial resistance. The
                                        Unidentified
                                                              Antimicrobial; styelin; microbial degradation; bactericide; viricide; fungicide; plant protection; styelin A; magainin 2.
                                                                                                                                12-MAY-2000
                                                                                                                                                        AAY67472;
                                                                                                                                                                                  AAY67472 standard;
                                                                                                                                                                                                                                                                                                                                                                            method is especially useful in preventing powdery mildew. The allows for levels of peptide expression to provide resistance phytopathogenic microbes without otherwise affecting the plant
                                                                                                     Magainin 2 partial peptide fragment.
                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 40; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antimicrobial peptides - comprising magainin and PGL classes peptides having an N-terminal methionine, used particularly for providing resistance in plants to pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blowers AD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SANF-) SANFORD SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                powdery mildew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antimicrobial peptide; resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAY-1999
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DB; AAX19274.
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                                                                                                                                                                                                                                                                                                   Similarity 92.1
12; Conservative
                                                                                                                                                                                                                                                   MGIGKFLHSAKKF
                                                                                                                                                                                                                                                                 IGIGKFLHSAKKF
                                                                                                                                                                                                                                                                                                                                                       39 AA;
                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sanford J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      localised antimicrobial magainin 2 peptide
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                                                                                                                                                                                 peptide;
                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                59.3%;
                                                                                                                                                                                                                                                  28
                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith
                                                                                                                                                                                                                                                                                                Score 64; DB
Pred. No. 0.00
1; Mismatches
                                                                                                                                                                                 19
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                                                                                                                                                                                                                                                                                                             DB 20;
0.0071;
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                                                                                                                                                                                                                                                                                                                           20;
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                                                                                                                                                                                                                                                                                                                           Length 39;
                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                              plant
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RESULT
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Best Local
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20-JAN-1998;
18-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to antimicrobial peptides (styelins) (and acetylated forms, salts, amides and esters of styelins), isolated from Styela clava and characterized by specific patterns of basic and hydrophobic amino acid side chains which display a broad spectrum of antimicrobial activities. The peptides are of a specified formula and display a wide range of antimicrobial activities and are therefore useful for preserving materials susceptible to microbial degradation, for protecting plants against bacterial infection and in the therapeutic and prophylactic protection of animals against bacteria, fungiand viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antimicrobial styelin peptides isolated from Styela clava useful preserving materials vulnerable to microbial degradation and for protecting plants and animals against pathogenic microbes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhao
                                                                                                                                                    04-MAR-1987;
                                                                                                                                                                                                                                                                                                                                                      synthetic
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WPI; 1987-334845/47
                                                                                                                                                                                                      04-MAR-1987;
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                                                                                                                                                                                                                                                                                                        USN7021493-N
                                                                                                                                                                                                                                                                                                                                                                                                           Magainin;
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01-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP71208;
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                                                  Zasloff MA;
                                                                                                  (USSH ) US DEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Magainin III polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP71208 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       including v.
magainin 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REGC )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e compounds may also be used as standards in antimicrobial assays and affinity ligands for absorption of counterpart structures in microbes, cluding viruses. The present sequence represents a partial fragment of gainin 2, used in comparison studies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ú
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIGKFLHSAKKF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIGKFLHSAKKF 20
                                                                                                                                                                                                                                                                                                                                                                                                             antimicrobial; antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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(first entry)
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98US-0072885.
98US-0075026.
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                                                                                               HEALTH & HUMAN
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To G1 is attached NH2 and to N22 is attached OH.

Magainins are a class of substantially pure, homogeneous
polypeptides composed exclusively of about 25 amino acids, having a
mol. wt. of about 2500 or less, being water soluble at a concentration
of greater than 5 mg/ml at neutral pH or in an aq. solution of
physiologic ionic strength. They are amphiphilic surface-seeking and have
                                                                                                                                                                                                                                                                                                                                                                                    Magainin polypeptide; cytotoxic agent; antimicrobial agent; therapeutic; antilleukaemia; AIDS; HTLV III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sol. and non-cytolytic to animal cells, incl. RBCs ,and is amphiphilic. It is an active antimicrobial agent being effective against both Gram-positive and -negative bacteria. It is also effective against fungi and protozoa. It is therefore useful as an antibiotic. See also AAP71206-07
                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fungi and protozoa. See also AAP71206-07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antimicrobial polypeptide cpds. - are positive and negative bacteria, fungi and
                                                                                                             -negative bacteria, fungi,
and spermicidal agents
                                                                                                                          New Magainin polypeptide(s) - active against Gram-positive and -negative bacteria, fungi, viruses and protozoa and as cytotox
                                                                                                                                                              WPI; 1988-105363/15
                                                                                                                                                                                      Zasloff
                                                                                                                                                                                                                                       05-AUG-1987;
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04-MAR-1987;
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                                                                                       Disclosure;
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10-DEC-1990
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87US-0021493.
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antitumour activity; contraceptive;
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Query Match
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                                                                 Analogues have the same activity as Megainin I and II coupled with insignificant haemolytic action against human red blood cells. Useful as antibiotics, fungicides, spermicicdes, in destroying tumors and as preservatives and in sterilisation of food etc.
                                                                                                                                        Deletion analogues of Magainin I and II peptide(s) - having high activity against microorganisms with low haemolytic action against human red blood cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a broad spectrum of properties at physiologic ionic strength and pH. The polypeptide is a microbial agent capable of inhibiting the growth or proliferation of gram-positive and gram-negative bacteria, fungi, virus and protozoan species. They are also useful as therapeutic cytotoxic agents. This includes antitumour activity. They are useful as spermicides and as a contraceptive agent. Magainin is active against HTLV III in vitro and has the potential to reduce the infectivity of the AIDS virus indicating its use as a serilant against the virus or as a chemotherapeutic agent for treating sterilant against the virus or as a chemotherapeutic agent for treating
                                                 Sequence
                                                                                                                        Claim 24;
                                                                                                                                                                                  WPI; 1990-209623/27.
                                                                                                                                                                                                         Cuervo
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                                                                                                                                                                                                                                                                                         14-JUN-1990
                                                                                                                                                                                                                                                                                                                                                    fungicide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            See also AAP82734-37.
                                                                                                                                                                                                       JH,
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                                                                                                                                                                                                                                                                                                                                                                                 analogue of Magainin
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                                                                                                                       Page 24;
                                                 22
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          Conservative
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RESULT 11
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                                                                   Magainin II; antibiotic;
                                                                                         Deletion analogue of Magainin
                                                                                                                 05-NOV-1990
                                                                                                                                         AAR05734;
                                                                                                                                                               AAR05734 standard;
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                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25;
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                                                        fungicide;
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                                                        preservant.
                                                                                                                                                                                                                                                                                                                       22 AA;
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                                                                                                                                                              protein;
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Analogues have the same activity as Megainin I and II coupled with insignificant haemolytic action against human red blood cells. Useful as antibiotics, fungicides, spermicicdes, in destroying tumors and as preservatives and in sterilisation of food etc.
                                                                       Deletion analogues of Magainin I and II peptide(s) - having high activity against microorganisms with low haemolytic action against human red blood cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deletion analogues of Magainin I and II peptide(s) - having high activity against microorganisms with low action against human red blood cells.
                                                    Claim 23;
                                                                                                                                       Cuervo
                                                                                                                                                                                09-DEC-1988;
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                                                                                                                                                                                                                                                                                      fungicide;
                                                                                                                                                                                                                                                                                                 Magainin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cuervo JH, Houghten RA;
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Pred. No.
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                                                                                                                                                                                                                                                                                                 cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11;
0.0057;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haemolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
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RESULT 13
AAR10658
ID AAR10
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Matches 12
                                                                                               The substitution analogue has biological activity equal to or greater than the parent Magainin II peptide. The analogue is effective as antibiotic and can be used to inhibit, prevent or destroy the growth or proliferation of microbes such as Grampositive and Grampegative bacteria, fungi, viruses and protozoa. It can also be used as a spermicide to inhibit, prevent or destroy the motility of sperm and as anti-tumour agent to inhibit the growth of or destroy tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Magainin I; antibiotic;
                                                                                                                                                                                                   Claim 26; Page 55; 58pp; English.
                                                                                                                                                                                                                               Substitution analogues of magainin I and II biological activity, useful as spermicide, ant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                              Sequence
                                                                                                                                                                                                                                                              WPI; 1991-051314/07.
                                                                                                                                                                                                                                                                                  Houghten RA,
                                                                                                                                                                                                                                                                                                                           07-JUL-1989;
                                                                                                                                                                                                                                                                                                                                              28-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                  24-JAN-1991.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Magainin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR10658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR10658
                                                                                                                                                                                                                                                                                                       (SCRI-) SCRIPPS CLINIC & RE
                                                                                                                                                                                                                       antitumour agents
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12; Conserv
...
                    9
                                      l Similarity
12; Conserv
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GIGKFLHSAKKF
                    GIGKFLHSAKKF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
                                                                              22
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                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                analogue (XII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                               A,
                                                                                                                                                                                                                                                                                  Cuervo JH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΑA;
                                                                                                                                                                                                                                                                                                                           89US-0376754.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 18..18
                                                                                                                                                                                                                                                                                                                                                                                                         /label= E-F-moc-lysine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.3%;
                                               58.3%;
12
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                                       0;
                                       Score 63; DB; Pred. No. 0.0
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Pred. No.
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                                       DB 12; 1
0.0057;
hes 0;
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0.0057;
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antibiotic, antiviral
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                                                         Length 22;
                                                                                                                      agent to inhibit
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                                         Indels
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                                         Gaps
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RESULT 14

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RESULT 15
AAR10642
ID AAR10
XX
AC AAR10
XC AAR10
DT 18-AP
XX
DE Magai
XX
Magai
KW Magai
KW Magai
KW Matib
XX
OS Synth
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ID AAR1
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XX
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XX
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                                                                                                                                                                                                                             Matches
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Best Local :
 Synthetic
                Magainin I; magainin II; substitution analogue; antibiotic; antiviral; antitumour.
                                                       Magainin
                                                                                                                                                                                                                                                                                      The substitution analogue has biological activity equal to or greater than the parent Magainin II peptide. The analogue is effective as antibiotic and can be used to inhibit, prevent or destroy the growth or proliferation of microbes such as Grampositive and Grampegative bacteria, fungi, viruses and protozoa. It can also be used as a spermicide to inhibit, prevent or destroy the motility of sperm and as anti-tumour agent to inhibit the growth of or destroy tumours.

See also AAR10639-47, AAR10657-63 and AAR10999.
                                                                           18-APR-1991
                                                                                                   AAR10642;
                                                                                                                      AAR10642 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                             Substitution analogues of magainin I and II - having increased biological activity, useful as spermicide, antibiotic, antiviral and antitumour agents
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 26; Page 55; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-051314/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Magainin I;
antibiotic;
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                                                                                                                                                                                           GIGKFLHSAKKF 20
                                                                                                                                                                               GIGKFLHSAKKF 12
                                                   II analogue (V).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          II analogue (IV).
                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                         58.3%; S ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         magainin II; substitution analogue; spermicide;
antiviral; antitumour.
                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cuervo JH;
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18..18
/label= G, A
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0.0057;
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                            spermicide;
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                      QY
                                                Query Match
Best Local S
Matches 12
                                                                                                                 The substitution analogue has biological activity equal to or greater than the parent Magainin II peptide. The analogue is effective as antibiotic and can be used to inhibit, prevent or destroy the growth or proliferation of microbes such as Grampositive and Grampegative bacteria, fungi, viruses and protozoa. It can also be used as a spermaicide to inhibit, prevent or destroy the motility of sperm and as anti-tumour agent to inhibit the growth of or destroy tumours. See also AAR10639-47, AAR10657-63 and AAR10999.
                                                                                                                                                                                                                                                Claim 26; Page 55; 58pp; English.
                                                                                                 Sequence
                                                                                                                                                                                                                                                                                     Substitution analogues of magainin I and II - biological activity, useful as spermicide, ant
                                                                                                                                                                                                                                                                            and antitumour agents
                                                                                                                                                                                                                                                                                                                             WPI; 1991-051314/07.
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Modified-site
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              9 GIGKFLHSAKKF 20
                                                Similarity
12; Conser
GIGKFLHSAKKF 12
                                                                                                 22 AA;
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                       Cuervo JH;
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                                            58.3%; Score 63; DB 100.0%; Pred. No. 0.0 tive 0; Mismatches
                                                                                                                                                                                                                                                                                     againin I and II - having increased as spermicide, antibiotic, antiviral
                                                         DB 12;
0.0057;
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Search completed: June 6, 2003, 13:23:38 Job time: 31.5 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         magainin precursor - African clawed frog
N;Contains: magainin 1; magainin 2
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change_18-Aug-2000
C;Accession: A28620; A29771
R;Terry, A.S.; Poulter, L.; Williams, D.H.; Nutkins, J.C.; Giovannini, M.G.; Moore, J. Biol. Chem. 263, 5745-5751, 1988
A;Title: The cDNA sequence coding for prepro-PGS (prepro-magainins) and aspects of ta;Reference number: A28620; MUID:88186892; PMID:2833514
A;Accession: A28620; MUID:88186892; PMID:2833514
                                                                                                                                                                                            recombination protein recA - Corynebacterium glutamicum N;Alternate names: recombinase A C;Species: Corynebacterium glutamicum C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 20-Apr-2001 C;Accession: I40728; S41939; I40727; S39258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-303 <TER>
A;Cross references: GB:J03193; NID:g214654; PIDN:AAA49930.1; PID:g214655
A;Cross references: GB:J03193; NID:g214654; PIDN:AAA49930.1; PID:g214655
R;Zasloff, M.
Proc. Natl. Acad. Sci. U.S.A. 84, 5449-5453, 1987
Proc. Natl. Acad. Sci. U.S.A. 84, 5449-5453, 1987
A;Title: Maggalinins, a class of antimicrobial peptides from Xenopus skin:
A;Reference number: A29771; MUID:87261003; PMID:3299384
A;Accession: A29771
A;Molecule type: mRNA
A;Residues: 6-73,'Q',75-158,297-303 <ZAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
A28620 .
            A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-376 <BIL1>
A;Cross-references: EMBL:X77384; NID:g475063; PIDN:CAA54563.1; PID:g475064
A;Experimental source: strain AS019
R;Billman-Jacobe, H.
                                                                                                           DNA Seq. 4, 403-404, 1994
A;Title: Nucleotide sequence of a recA gene from Corynebacterium glutamicum. A;Reference number: I40728; MUID:95143581; PMID:7841463
A;Accession: I40728
                                                                                                                                                                                                                                                                               RESULT
I40728
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12; Conserv
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B81258
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S75388
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Pred. No.
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0.012;
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47.5 47.5 47.5 47.4

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Database

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Post-processing: Minimum Match 0%

Listing

Match

Maximum Minimum

DB

seq

length: 0 length: 2000000000

Searched:

283224 seqs, Gapop 10.0 ,

Scoring table: Sequence: Perfect score:

BLOSUM62

108

US-10-081-418-1

Run on: OM protein -

June

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R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
C75035
                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-237 <K
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R; Fitzpatrick, R.; O'Donohue, M.; JOy, J.; Heery, D.M.; Dunican, Appl. Microbiol. Biotechnol. 42, 575-580, 1994
A; Title: Construction and characterisation of recA strains of Cor A; Reference number: 140727; MUID:95134369; PMID:7765733
                                                                                                                                                                                                                 A; Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                          A; Reference number: A75001
A; Accession: C75035
                                                                                                                                                                                                                                                                                                                                                              A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arginase related protein PAB1539 [imported] - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description: plays an essential role in homologous recombination, C; Superfamily: recombination protein recA C; Keywords: ATP; DNA binding; DNA recombination; DNA repair; nucleot F; 78-85/Region: nucleotide-binding motif A (P-loop) F; 152-157/Region: nucleotide-binding motif B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 118-132,'I',134-169,'GN',172-190,'S',192-200 <FIT1>
A;Cross-references: EMBL:X75085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X75085; NID:g474416; PIDN:CAA52977.1; PID:g474417
R;Fitzpatrick, R.; O'donohue, M.; Joy, J.; Heery, D.M.; Dunican, L.K.
submitted to the EMBL Data Library, September 1993
A;Description: Construction and characterisation of recA strains of Corynel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: I40727
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A; Residues: 1-102, 'DSF', 106-376 <BIL2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: Nucleotide sequence of A; Reference number: S41939
A; Accession: S41939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 118-200 <FIT2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Species: Pyrococcus abyssi;Date: 20-Aug-1999 #text_change;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change
                                                                                                                                                                                                                                   ;Cross~references: GB:AJ248287; GB:AL096836;
                                                                                    Matches
                                                                                                                            Query Match
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                                                                                                                                                                                                                                                         1-237 <KAW>
                                                                                    Similarity 9; Conserv
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KWKAYINLKQHGMGRVIREARKF 157
                                        KWKLF---KKIGIGKFLHSAKKF 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLFKKIGIGKF 13
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                                                                                                      44.0%;
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                                                                              Pred. No. 3.5, 6; Mismatches
                                                                                                    Score 47.5;
Pred. No. 3
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Pred. No. 4.7;
4; Mismatches
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                                                                                                                                                                                                                                   PIDN:CAB50176.1;
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RESULT 4

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A; Rolecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1562 < DEL>
A; Residues: 1-268 < EMBL: 268906; NID: e989397; PID: e219958;
A; Cross references: EMBL: 268906; NID: e989397; PID: e219958;
A; Cross references: strain SAS56; clone bc-atra
                                                                                                                                C;Accession: T43022
R;Del Sorbo, G.; Andrade, A.C.; Van Nistelrooy J, G.M.; Van Kar Mol. Gen. Genet. 254, 417-426, 1997
A;Title: Multidrug resistance in Aspergillus nidulans involves A;Reference number: Z07910; MUID:9180695; PMID:9180695
A;Accession: T43022
                                                                                                                                                                                                                                                          ATP-binding multidrug cassette transport protein - Botryotinia fuckeliana C;Species: Botryotinia fuckeliana C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                 RESULT
T43022
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T50950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein B24P7.50 [imported] - Neurospora crassa C;Species: Neurospora crassa C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_cha
                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                         ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 6
A; Introns: 30/3; 235/2
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submitted to the Protein S
A;Reference number: Z25286
A;Accession: T50950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A83650; MUID:20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein BH4041 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: A84155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AL389890; GSPDB:GN00116; NCSP:B24P7.50
A;Experimental source: BAC clone B24P7; strain OR74A
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A; Residues: 1-491 <SCH>
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A;Experimental source: strain C-125
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A; Residues: 1-427 <STO>
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Best Local Similarity
Matches 10; Conserv
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Pred. No. 7.
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Pred. No. 6
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                                              PIDN:CAA93142.1
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A;Title: Identification and genetic analysis of normal and mutant phytoene synthase general A;Accession: S35154; MUID:93344508; PMID:8343597
A;Status: translation nor -
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N,Alternate names: ripening protein 5

C;Species: Lycopersicon esculentum (tomato)

C;Cate: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 02-Mar-2001

C;Cacession: S22474; S06321; S35155; S35154; S21981; S24967; S24968

R;Ray, J; Moureau, P; Bird, C.; Bird, A.; Grierson, D.; Maunders, M.; Truesdale, M.; Elant Mol. Biol. 19, 401-404, 1992

A;Title: Cloning and characterization of a gene involved in phytoene synthesis from toma A;Reference number: S22474, MUID:92322971; PMID:1623189

A;Rocession: S22474

A;Molecule type: DNA

A;Residues: 1-412 <RAYY

A;Residues: 1-412 <RAYY
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A;Introns: 188/3; 338/3; 655/3; 711/2; 814/1; 1356/3
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding
                                                                                                                                                                                                                                                                                                                                             A:Experimental source: mutant r
C;GenetLcs:
A;Gene: Psyl
A;Introns: 138/1; 155/1; 212/3; 291/2; 355/3
C;Superfamily: Mycobacterium marinum phytoen
C;Keywords: chloroplast; transferase
                                                   RESULT
A42102
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A;Residues: 1-107,'VECLESDPLOTERTGVSLPGORVGGSRGAT','RWPGGPGGRRRGADGIQCCCIGPLIFC' <FRA2>
A;Cross-references: EMBL:X67143; NID:g19398; PIDN:CAA47624.1; PID:g19399
A;Experimental source: mutant r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X60441; GB:S39572; NID:g19248; PIDN:CAA42969.1; PID:g19249 A;NOte: the authors did not translate the codon for residue 155 R;Ray, J.; Bird, C.; Maunders, M.; Grierson, D.; Schuch, W. Nucleic Acids Res. 15, 10587, 1987 A;Title: Sequence of pTOM5, a ripening related cDNA from tomato. A;Reference number: S06321; MUID:88096591; PMID:3697097 A;Accession: S06321
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A;Experimental source: mutant rY
A;Accession: S35154
A;Status: translation not shown
phytoene synthase (EC 2.
C; Species: Lycopersicon
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A; Residues: 1-387, 'NMI
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Residues: 1-406,'N',408-412 <RAY1>
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les 8; Conserv
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2.5.1.-) peripheral plastid on esculentum (tomato)
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Pred. No.
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Pred. No.
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                                                                                                                                                                                     C;Species: Hyalophora cecropia (cecropia moth)
C;Date: 24-Sep-1981 #sequence_revision 04-Nov-1994 #text_change 18-Jun-1999
C;Accession: A40A20; S00208; A91121; A93260; A01769
R;Gudmundsson, G.H.; Lidholm, D.A.; Asling, B.; Gan, R.; Boman, H.G.
J. Biol. Chem. 266, 11510-11517, 1991
A;Title: The cecropin locus. Cloning and expression of a gene cluster encod. A;Reference number: A40420; MUID:91268009; PMID:1711035
A;Accession: A40420
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G90566
                                           R; Lidholm, D.A.; Gudmundsson, FEBS Lett. 226, 8-12, 1987 A; Title: Insect immunity; cDN:
                                                                                         A;Molecule type: DNA
A;Residues: 1-64 <GUD>
A;Residues: 1-64 <GUD>
A;Cross-references: GB:M63845; NID:g159196; PIDN:AAA29185.1; PID:g159197
A;Cross-references: GB:M63845; NID:g159196; PIDN:AAA29185.1; PID:g159197
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A; Reference number: A; Accession: S00208
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S00208

cDNA clones

coding for the

precursor

forms

of cecropins

encoding

three

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C;Date: 04-Mar-1993 *seq
C;Accession: A42102
R;Bartley, G.E.; Viitane
J. Biol. Chem. 267, 5036
A;Title: A tomato gene e
A;Reference number: A421
                                                                                                                                                                                                                                                                                                                                                                                                       R;Chambaud, I.; Heilig, N., 2001
R;Chambaud, I.; Heilig, N., 2001
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory
A;Title: The complete genome sequence of the murine respiratory
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A;Molecule type: mRNA
A;Residues: 1-412 <BAR>
                                                                                                                                                                                                                                                                   A;Gene: MYPU_4390
A;Genetic code: SGC3
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A; Residues: 1-666 < KUR>
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               cecropin A precursor - cecropia moth
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9; Conserv
names: cecropin
                                                                                                                                                                                         Similarity
9; Conserv
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                                                                                                             KHKIFKKIGLGFYSYIFEK 368
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67, 5036-5039, 19
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MUID:92184738;
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Pred. No.
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A;Molecule type: DNA
A;Residues: 1-925 <KUR>
A;Cross-references: GB:AE008918; PIDN:AAL54192.1;
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A;Molecule type: protein
A;Residues: 27-63 <STED
R;Andreu, D.; Merrifield, R.B.; Steiner, H.; Boman, H.G.
Proc. Natl. Acad. Sci. U.S.A. 80, 6475-6479, 1983
A;Title: Solid-phase synthesis of cecropin A and related peptides.
A;Reference number: A54960; MUID:84042494; PMID:6579533
A;Reference number: A54960; MUID:84042494; PMID:6579533
A;Contents: annotation; chemical synthesis
A;Note: protein carboxyl-terminal composition and amidation determined by mass spectrome
C;Comment: Cecropins are a family of basic peptides having lytic and antibacterial activ
                                          В
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C; Keywords: oxidoreductase
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R;Hultmark, D.; Engstrom, A.; Bennich, H.; Kapur, R.; Boman, H.G.
Eur. J. Biochem. 127, 207-217, 1982
A;Title: Insect immunity: isolation and structure of cecropin D and four minor antibacte A;Reference number: A91121; MUID:83053366; PMID:7140755
A;Accession: A91121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, .; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nitrate reductase (EC 1.7.99.4) [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
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A;Title: Sequence and specificity of two antibacterial proteins involved A;Reference number: A93260; MUID:81245158; PMID:7019715
A;Accession: A93260
                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: BMEII0950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: strain 16M
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A;Accession: AE3628
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A;Residues: 27-64 chull
A;Residues: 27-6
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A; Residues: 1-64 <LID>
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Keywords: amidated carboxyl end; antibacterial; hemolymph; 1-22/Domain: signal sequence #status predicted <SIG>;23-26/Domain: propeptide #status predicted <PRO>;23-26/Domain: propeptide #status experimental <MAT>;27-63/Product: cecropin A #status experimental <MAT>;
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                                          72
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                                                                                                                1 KWKLFKKIGIGKFLHSAKKF 20
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                                          KWNLEEKDGKGKDVELAKSF 91
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                                                                                                                                                                                             Conservative
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50.0%;
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100.0%; Pr
0;
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Pred. No.
                                                                                                                                                                                                                                Score 45; DE Pred. No. 37;
                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                               Length 925;
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RESULT 13
S65297
                                                               F;118-134/Domain: transmembrane #status predicted <TM4>F;143-159/Domain: transmembrane #status predicted <TM5>F;143-159/Domain: transmembrane #status predicted <TM65>F;189-205/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:BA000018; PID:g13701522; PIDN:BAB42816.1; A;Experimental source: strain N315 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
C89957
                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-353 <DEL>
                                                                                                                                                                                                                                                                                                                                               R; Delius, H.; Hebling, U. submitted to the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Duesterhoeft, A.; Floeth, M.; Fritz, M.; Hilbert, H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Saccharomyces cerevisiae
C;Date: 10-Dec-1994 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable membrane protein YPL264c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein P0373
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A; Residues: 1-205 < KUR>
                                                                                                                                  F;96-112/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                  F;16-32/Domain:
                                                                                                                                                                                                   A;Cross-references: SGD:S0006185
A;Map position: 16L
                                                                                                                                                                                                                                                   A;Cross-references: EMBL:Z73620; NID:g1370544; PID:e246970; PID:g1370545; MIPS:YPL264
A;Experimental source: strain S288C (AB972)
                                                                                                                                                                                                                                                                                                              A; Accession: S65318
                                                                                                                                                                                                                                                                                                                                A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:Z73620; NID:g1370544; PID:e246970;
A;Experimental source: strain S288C (AB972)
                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-353 <DUE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A; Accession: S65297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the Protein Sequence
                                                                                                                                            ;16-32/Domain: transmembrane #status predicted
;54-70/Domain: transmembrane #status predicted
                                                                                                                                                                                  Keywords: transmembrane protein
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 Matches
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Similarity 7; Conserv
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46.78;
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                                  Length 353;
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B
Search completed: June 6, 2003, 13:25:26 Job time: 14.5 secs
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                                                                                                                                                                                                                                                                                   C;Superfamily: cecropin
C;Keywords: amidated carboxyl end; antibacterial
F;35/Modified site: amidated carboxyl end (Leu)
                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 1-35,'S' <QUX>
A;Note: the carboxyl end is blocked and was not sequenced directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Craig, A.G.; Engstroem, A.; Bennich, H.; Kamensky, I. Blomed. Environ. Mass Spectrom. 14, 669-673, 1987
A;Title: Plasma desorption mass spectrometry coupled with conventional peptide sequencing A;Reference number: A54725; MUID:88108273; PMID:2962676
A;Accession: A54725
                                                                                                                                                                                                                                                                                                                                                                                                                               R;Qu, X.; Steiner, H.; Engstrom, A.; Bennich, H.; Boman, H.G. Eur. J. Blochem. 127, 219-224, 1982
A;Title: Insect immunity: isolation and structure of cecropins B and D from pupae of the A;Reference number: A91122; MUID:83053368; PMID:6754375
A;Accession: A01771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cecropin B - Chinese oak silkmoth
(;Species: Antheraea pernyi (Chinese oak silkmoth)
C;Date: 17-Dec:1982 #sequence_revision 12-Apr-1996 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 1-35 < CRA>
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A;Authors: Squres, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable plcA protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:283860; GB:AL123456; NID:g3261681; PIDN:CAB06148.1; PID:g1781258
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                          Query Match
Best Local Similarity 87.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: H70662
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Best Local 9
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nes 5; Conserv
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                                                                                                                             1 KWKLFKKI 8
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Pred. No. 2
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Maximum Match 100%
Listing first 45 summaries
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Sequence:
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        Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
      Score
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Match
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Gapop 10.0 , Gapext 0.5
    112892 seqs, 41476328 residues
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108
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Copyright (c) 1993 - 2003 Compugen
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(Without alignments)
118.504 Million cell updates/sec
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RECA_CORGL
PSY1_LYCES
CECA_HYACE
PHIA_MYCTU
CECB_ANTPE
YKL1_CAEEL
WTD3_STYHU
VNUC_INCCA
Y870_METJA
GALX_SCHPO
CECB_HYACE
CECA_BOWIN
KC1A_BOWIN
KC1A_CHICK
KC1A_CHICK
KC1A_CHICK
KC1A_CHICK
KC1A_HUMAN
APKA_ARATH
ARLY_BUCAI
BLA1_HAEIN
KC1B_BOVIN
SY1_SULAC
NKX3_MOUSE
CNEX3_MOUSE
CNEX3_MOUSE
CNEX3_HOME
PCD8_DROME
CECB_BOMMO
CE3D_HYPCU
CECB_BOMMO
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P42442 corynebacte
P424442 corynebacte
P424442 corynebacte
P424442 corynebacter
P424462 corynebacter
P42464 corynebacter
P42507 hyalophora
Q40101 mycobacter
P41508 caenorhabdi
Q43138 stylosanthe
P68028 influenza c
Q58280 methanococc
Q9hdu3 schizosacch
P61508 hyalophora
Q27239 bombyx mori
P44279 haemophilus
P35506 bos taurus
P97633 rattus norv
P70065 gallus gall
P48729 homo sapien
P95960 sulfolobus
Q9hc58 homo sapien
P95965 homo sapien
Q06548 arabidopsis
P57159 buchnera ap
P33507 bos homophilus
P57159 buchnera
            Q9vq79
P14666
P50720
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8 homo sapien
9 dengue viru
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Varins S.M., Fitzpatrick R
                                                            Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteria (class); Actin
Actinomycetales; Corynebacterineae; Corynebacteriaceae;
                                                                                        RECA_CORGL STANDARD; PRT; 376 AA. p42442; O1-NOV-1995 (Rel. 32, Created) O1-NOV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) RecA protein (Recombinase A).
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pair of basic residues; Repeat; Amphibian skin; Fungicide; Hemolysis; Signal; 3D-structure.
18 POTENTIAL.
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01-AUG-1988
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15-JUN-2002
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submitted (MAY-2002)
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P08196;
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EMBL; X75085; CAA52977.1; -.
HSSP; P26345; 1G19.
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PROSITE; PS50162; RECA_2; 1.
PROSITE; PS50163; RECA_3; 1.
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ProDom; PD000229; RECA; 1.
SMART; SM00382; AAA; 1.
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InterPro; IPR001553; RecA.
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EMBL; A21360; CAA01548.1; --
PIR; S06321; S06321;
PIR; A42102; A42102;
InterPro; IRP002060; Squ/phyt_
Pfam; PF00494; SQS_PSY; 1.

Pfam; PF00494; SQUALEN_PHYTOEN_SYN_1; 1.

PROSITE; PS01044; SQUALEN_PHYTOEN_SYN_2; 1.

Multifunctional enzyme; Carotenoid blosynthesis;

Isoprene blosynthesis; Transferase; Chloroplast;
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"Cloning and characterization of a gene involved in phytoene synthesis from tomato.";
Plant Mol. Biol. 19:401-404(1992).

- Plant Mol. Biol. 19:401-404(1992).
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MEDLINE-88096591; PubMed-3697097;
RAY J., BHIC C.R., Maunders M., Grierson
"Sequence of pTOM5, a ripening related of
Nucleic Acids Res. 15:10587-10587(1987).
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MEDLINE=94071905; PubMed=8250898;
Roemer S., Hugueney P., Bouvier F.
"Expression of the genes encoding enzymes in Capsicum annuum.";
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J. Blol. Chem. 267:5036-5039(1992).
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STRAIN-cv. Ailsa Craig;
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PATHWAY: Carotenoid biosynthesis.
SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Chloroplast.
DEVELOPMENTAL STAGE: IN SEEDLINGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TO PHYTOENE.

CATALYTIC ACTIVITY: 2 ge
prephytoene diphosphate
CATALYTIC ACTIVITY: Prep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDUCTION: BY FRUIT RIPENING.
SIMILARITY: BELONGS TO THE PHYTOENE/SQUALENE SYNTHETASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Res. Commun. 196:1414-1421(1993).
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protein pTOM5).
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                 Multigene family;
Transit peptide.
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RESULT 4
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                            SEVERAL GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIAL
-!- SUBCELLULAR LOCATION: Secreted.
-!- PIM: A PROTEIN WITH THE SAME SEQUENCE AS CECROPTM
THE CARROXYL BICCOUNTY
                                                                      Holak T.A., Engstroem A., Kraulis P.J., Lindeberg G., Bennich Jones T.A., Gronenborn A.M., Clore G.M.;
Jones T.A., Gronenborn A.M., Clore G.M.;
"The solution conformation of the antibacterial peptide cecro nuclear magnetic resonance and dynamical simulated annealing Biochemistry 27:7620-7629(1988).

1- FUNCTION: CECROPINS HAVE LYTIC AND ANTIBACTERIAL ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-91268009; PubMed-1711035; Gan R., Gan R., Boman H.G. Gudmundsson G.H., Lidholm D.-A., Aasling B., Gan R., Boman H.G. "The cecropin locus. Cloning and expression of a gene cluster encoding three antibacterial peptides in Hyalophora cecropia."; J. Biol. Chem. 266:11510-11517(1991).
                                                                                                                                                                                                                        PRELIMINARY SEQUENCE OF 27-63.
MEDLINE-81245158; PubMed-7019715;
Steiner H., Hultmark D., Engstroem A., Bennich H., Bomar "Sequence and specificity of two antibacterial proteins".
                                                                                                                                                                                                                                                                                           Hultmark D., Engstroem A., Bennich H., Kapur "Insect immunity: Isolation and structure of minor antibacterial components from Cecropia Eur. J. Biochem. 127:207-217(1982).
                                                                                                                                                                                                                                                                                                                                                                                          Lidholm D.-A., Gudmundsson G.H., Xanthopoulos K.G., "Insect immunity: cDNA clones coding for the precurs cecropins A and D, antibacterial proteins from Hyald FEBS Lett. 226:8-12(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hyalophora cecropia (Cecropia moth).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Chirysia; Bombycoidea; Saturniidae; Saturniinae; Attacini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1988 (Rel. 07, Last sequence up 15-JUN-2002 (Rel. 41, Last annotation Cecropin A precursor (Cecropin C).
                                                                                                                                                          STRUCTURE BY NMR. MEDLINE=89088132; PubMed=3207693;
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MEDLINE-83053366; PubMed-7140755;
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THE CARBOXYL BLOCKING GROUP, REF.3 AUTHORS.
SIMILARITY: BELONGS TO THE C
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PHYTOENE SYNTHASE 1.

KLIALPIAYAKSLYPPTKY ->

QVDCITYCICKISCASYKN (IN REF. 3)

KLIALPIAYAKSLYPPT ->

QVDCITYCICKISCASY (IN REF. 4).
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the precursor forms of
s from Hyalophora cecro
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                      BUT LACKING CECROPIN C
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Glossata;
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Matches
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EMBL; X063845; AAA29185.1; -.
PIR; A01769; CKWKA.
PIR; A040420; A40420.
PIR; S00208; S00208.
InterPro; IPR000875; Cecropin.
InterPro; IPR003254; IIP_Cecropin.
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entities requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
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between
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01-NOV-1997 (Rel. 35, Created) 
16-OCT-2001 (Rel. 40, Last sequence update) 
16-OCT-2001 (Rel. 40, Last annotation update) 
Phospholipase C 1 precursor (EC 3.1.4.3) (MTP40 
PLCA OR MPCA OR MTP40 OR RV2351C OR MT2416 OR MT
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MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.
                                                                                                                                                                                                                    Leao S.C., Rocha C.L., Murillo L.A., Parra C.A., Patarroyo M.E.;
"A species specific nucleotide sequence of Mycobacterium tuberculosis encodes a protein that exhibits hemolytic activity when expressed in Escherichia coli.";
                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                               Actinomycetales;
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteria (class);
Actinomycetales; Corynebacterineae; Mycobacteriace
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                                                     SEQUENCE FROM STRAIN-H37Rv;
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                                                                                                                                                                                                                                                                                         STRAIN-H37Rv;
                                    MEDLINE=98295987;
                                                                                          Tohansen K.A., Gill R.E., Vasil M.L., "Johansen K.A., Gill R.E., Vasil M.L., "Blochemical and molecular analysis of phospholipase pactivity in mycobacteria."; Infect. Immun. 64:3259-3266(1996).
                                                                                                                                                                   STRAIN-H37Rv;
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Mycobacteriaceae; Mycobacterium
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There are no restrictions

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Wera-Cabrera I., Howard S.T., Lasslo A., Johnson W.M.;

"Analysis of genetic polymorphism in the phospholipase re
mycobacterium tuberculosis.";

J. Clin. Microbiol. 35:1190-1195(1997).

-1- FUNCTION: HYDROLYZES SPHINGOMYELIN IN ADDITION TO
pHOSPHATIDYLCHOLINE. PROBABLE VIRULENCE FACTOR IMPLIC
PATHOGENESIS OF M. TUBERCULOSIS AT THE LEVEL OF INTRAC
SURVIVAL, BY THE ALTERATION OF CELL SIGNALING EVENTS
CYTOTOXICITY.

-1- CATALYTIC ACTIVITY: A phosphatidylcholine + H(2)0 = 1
diacyjglycerol + choline phosphate.
-1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED; AT THE EXT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CDC 1551 / Oshkosh; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White C Fleischmann R.D., Alland D., Eisen J.A., Ermolaeva M.D., Hickey Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzbe Belcher B., Utterback T., Weidman J., Khouri H., Gill J., Miku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91372944; PubMed=1909999;
Parra C.A., Londono L.P., del Portillo P., Patarroyo M.E.;
"Isolation, characterization, and molecular cloning of a sy
Mycobacterium tuberculosis antigen gene: identification of
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SIMILARITY: BELONGS TO THE BACTERIAL PHOSPHOLIPASE C CAUTION: REF. 5 AND REF. 6 SEQUENCE DIFFERS FROM THAT SCREEN
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SWISS-PROT entry is copyright. It is produced through
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RA MEDLINE-88108273; PubMed=2962676;
RT Plasma desorption mass spectrometry coupled with conventional repetide sequencing techniques.";
RT Peptide sequencing techniques.";
RL Biomed. Environ. Mass Spectrom. 14:669-673(1987).
CC PERECTION: CECROPINS HAVE LYVIC AND ANYIBACTERIAL ACTIVITY AGAINST CC SEVERAL GRAW-POSITIVE AND GRAM-NEGATIVE BACTERIA.
CC I- SUBCELLULAR LOCATION: Secreted.
CC I- SUBCELLULAR LOCATION: Secreted.
CC I- SIMILARITY: BELONGS TO THE CECROPIN FAMILY.
DR PIR; A01771; CKAOBP.
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DR InterPro; IPR003254; IIP_cecropin.
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DR PFO0275; CECROPIN; 1.
DR PROSITE; PS003268; CECROPIN; 1.
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MEDLINE-83053368; PubMed-6754375;

Qu X.-M., Steiner H., Engstroem A., Bennich H., Boman H.

"Insect immunity: isolation and structure of cecropins B

pupae of the Chinese oak silk moth, Antheraea pernyi.";

Eur. J. Blochem. 127:219-224(1982).
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Eukaryota; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
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15-DEC-1998
                               Stylosanthes humilis (Townsviile stylo). Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicote; Rostdeurosids I; Fabales; Fabaceae; Papilionnideae. Nacohumomoronicalis de la contraction de la contraction
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                                                                                                                                                                   CAD3.
                                                                                                                                                                                              mannitol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                  MTD3_STYHU
Q43138;
                                                                                                                                                                                                                                                                                                                                                                                                                                    STYHU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00107;
PROSITE; PS00108;
PROSITE; PS50011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 235637; CAA84685.1; -. HSSP; Q06486; 1CKI. WormPep; C03C10.1; CE00872.
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative casein kinase I C03C10.1 in chromosome
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InterPro; IPR002290; Ser_thr_pkinase.
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                                                                                                                                                                             1. 37, Created)
1. 37, Last sequence update)
1. 37, Last annotation update
21 dehydrogenase 3 (EC 1.1.1.
2 ogenase 3).
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PROTEIN_KINASE_ST; 1.
PROTEIN_KINASE_DOM; 1.
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61.5%;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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W; 17AD6E173551BABC CRC64;
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                           Papilionoideae;
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                           Aeschynomeneae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 341;
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P08028;
01-AUG-1988
01-AUG-1988
01-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nourse J.P., Manners J.M., Curtis M.D., Abrahams S.L., Watson J.M.;
Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.

Submitted (NOV-1994) to TO MANNOSE PROVIDES THE INITIAL STEP
BY WHICH TRANSLOCATED MANNITOL TO MANNOSE PROVIDES THE INITIAL STEP
BY WHICH TRANSLOCATED MANNITOL IS COMMITTED TO CENTRAL METABOLISM
AND, BY REGULATING MANNITOL POOL SIZE, IS IMPORTANT IN REGULATING
SALT TOLERANCE AT THE CELLULAR LEVEL (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: D-mannitol + NAD(+) = D-mannose + NADH.
-!- COPACTOR: ZINC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INCCA
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                       This
                                                              MEDLINE=85170522; PubMed=6532006;
Nakada S., Creager R.S., Krystal M., Pal
"Complete nucleotide sequence of the inf
nucleoprotein gene.";
Virus Res. 1:433-441(1984).
-!- FUNCTION: ENCAPSIDATES THE NEGATIVE
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InterPro; IPR002085; Adh_zn_family.
Pfam; PF00107; adh_zinc; 1.
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                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  Viruses; ssRNA negative-strand Influenzavirus C.
                                                                                                                                                                                                                                                                                                                                                           Nucleoprotein.
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                                                                                                                                                                                                                                                                                                                 Influenza C virus
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Last annotation updat
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ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (SECOND ATOM) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).
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                                                                                                                                    Palese P.;
influenza
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                                                                   STRAND VIRAL RNA.
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                                                                                                                                       C/California/78
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Best Local
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01-NOV-1997
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-AL-1 / DSM 2661 / ATCC 43067;

MEDLIND-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaile B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus

jannaschii.";
                                                                                                                              EMBL; U67531; AAB98876.1;
HSSP; Q45560; 1BWE.
TIGR; MJ0870;
                                                                                                                                                                                                                                                                                                                              SCIENCE 273:1058-1073(1996).

-i- SIMILARITY: TO COENZYME F420 HYDROGENASE BETA SUBUNIT.
-i- SIMILARITY: TO M.JANNASCHII MJ1349, MJ0725 AND MJ0551.
-i- SIMILARITY: THE C-TERMINAL DOMAIN IS A 4FE-4S/SIROHEME DOMAIN
-i- SIMILARITY: THE C-TERMINAL DOMAIN IS A 4FE-4S/SIROHEME DOMAIN
FOUND IN NITRITE REDUCTASES (EC 1.6.6.4 AND EC 1.7.7.1) AND
SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.8.7.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M17700; AAA43798.1; -. PIR; S07413; VHIVC8.
                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                 use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleoprotein
                                                                                                                                                                                                                                                                 the European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   r870_metja
                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMPL outstation European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KWIMEKHIGIGVLIADAK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KWKLFKKIGIGKFLHSAK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       565 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein MJ0870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22C10CCB1A85AA84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.
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                                                                                                                                                                                                                                   Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                        commercial
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Pfam; PF00037; fer4; 3.
pfam; PF01077; NIR_SIR; 1.
pfam; PF03460; NIR_SIR_ferr;
PRINTS; PR00397; SIROHAEM.

PS00198;

4FE4S_FERREDOXIN;

InterPro; IPR000660; InterPro; IPR005117;

Nir_sir_fer 4Fe4S_ferredoxin.

InterPro; IPR001450;

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RESULT 11
GALX_S
AC 09HDU3
DT 15-JUN
DT 15-JUN
DT 15-JUN
DE (EC 5.
DE (Mutar
GAL10
OS Schizo
OC SCHIZO
RN (1)
RA STOUEN
RA GOOLII
                                       RA WOOD V. Gwilliam R. Rajandream M.A. Lyne M. Lyne R. Stewart A. Ra Sgouros J. Peat N. Hayles J. Baker S., Basham D. Bowman S., Ra Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., RA Gontles S., Goble A., Hamiln N., Harris D., Hddigo J., Hodgson G., RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hodgson G., RA Holroyd S., Monses L., Jones M., Leather S., McDonald S., McLean J., Semes K., Jones L., Jones M., Leather S., McDonald S., McLean J., Semes K., Jones L., Jones M., Leather S., McDonald S., McLean J., Semes K., Jones M., Leather S., McDonald S., McLean J., Semes K., Jones K., Ra James K., Jones M., Leather S., McDonald S., McLean J., Semes K., Stevens K., Ra Ratherford K., Rutter S., Saunders D., Seeger K., Sharp S., Stevens K., Stevens K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00365; N
Hypothetical protesic
Complete proteome.
METAL 428
METAL 434
METAL 468
METAL 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAL10 bifunctional protein [Includes: UDP-glucose 4-epimerase (EC 5.1.3.2) (Galactowaldenase); Aldose 1-epimerase (EC 5.1.3.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21848401; PubMed-11859360; Wood V., Gwilliam R., Rajandream M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAL10 OR SPBPB2B2.12C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GALX_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                рэнриз;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hes .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LFKKIGIGKFLHSAKK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VMKRVGYGKFLEEVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           620
                        Galactose metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428
434
468
472
metabolism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               613
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W; 9D71D2580D7D0BAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                     step
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB
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Boman

Proc. cecropin

"Molecular cloning, cDNA sequencing, and chemical cecropin B from Hyalophora cecropia."; Proc. Natl. Acad. Sci. U.S.A. 82:2240-2243(1985).

SEQUENCE

N.A

MEDLINE-86005745;

PubMed=3840100;

SEQUENCE FROM N.A. MEDLINE-85190472;

van Hofsten P., Faye

PubMed=3857578; aye I., Kockum K.,

Boman H.G.,

Engstroem A.,

Lee J.-Y., X

Xanthopoulos

synthesis

Boman H.G., Faye I., von Hofsten P., Xanthopoulos K.G., Bennich H., Engsti

Engstroem A.,

Kockum K., Lee J.-Y., roem A., Merrifield R.B.,

Xanthopoulos Andreu D.;

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ALD DE COMPANIA DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
CECB_HYACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP_BIND
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CECB_HYACE
P01508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The structure of the gene for cecropin protein from Hyalophora cecropia."; Eur. J. Biochem. 172:371-376(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; O
Ditrysia; Bombycoidea; Saturniidae; Saturniinae; Attacini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-88166708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hyalophora cecropia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cecropin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel.
13-AUG-1987 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001823; Ald1_epimerase.
InterPro; IPR001509; Epimerase_Dh.
InterPro; IPR000205; NAD_binding.
Pfam; PF012763; Aldose_epim; 1.
Pfam; PF01370; Epimerase; 1.
TIGRPAMS; TIGR01179; galE; 1.
PROSITE; PS00545; ALDOSE_1_EPIMERASE; 1.
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EPIMERASE FAMILY.
-!- SIMILARITY: IN THE C-TERMINAL SECTION;
EPIMERASE FAMILY.
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9; Conser
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350 GALACI
713 MUTARC
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05, Last sequence up
41, Last annotation
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80666 MW;
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NO. 32;
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CECA_BOMMO
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       CCC RTAR RD ROX OCC RTT RANK CCC
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Best Local S
Matches 7
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EMBI; M27404; CAA30306.1; ...
EMBI; M34924; AAA29187.1; ...
PIR; A01770; CKWKB.
PIR; S02606; S02506.
InterPro; IPR000875; Cecropin.
InterPro; IPR003254; IIP_cecropin.
PfAm; PF00772; Cecropin; 1.
PRODOM; PD003956; IIP_cecropin; 1.
PROSITE; PS00268; CECROPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                   Q27239;
01-NOV-1997
01-NOV-1997
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Hyalophora
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MEDLINE=81245158; PubMed=7019715;
                                                                                                                                                                                                 Bombyx mori (Silk moth).

Bukaryota; Metazoa; Arthropoda; Mandibulata;

Insecta; Pterygota; Neoptera; Endopterygota;

Ditrysia; Bombycoidea; Bombycidae; Bombyx.

NCBI_TaxID=7091;
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"Sequence and specificity of two antibacterial proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Steiner H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
Yamano Y., Matsumoto M., Inoue K., Kawabata T., Morishin "Cloning of cDNAs for cecropins A and B, and expression in the silkworm, Bombyx mori.";
Biosci. Biotechnol. Biochem. 58:1476-1478(1994).
                                                                                                                                                                                                                                                                                                                                           Cecropin A precursor.
                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
                                                                                                           STRAIN=C108; TISSUE=Larval fat bo
MEDLINE=94369101; PubMed=7765280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CECA_BOMMO
                                                                                                                                                              SEQUENCE FROM N.A.
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Pred. No.
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65E309CB2983BD61
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Lepidoptera; (
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                                                          Morishima 1.,
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GN H11631
OS Haemog
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-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN FAT BODY AND HEMOCYTES.
-!- TIS ALSO EXPRESSED IN MALPICHIAN TUBE AND TO A MUCH LESSER EXTENT IN MIDGUT. NOT PRESENT IN SILK GLAND.
-!- SIMILARITY: BELONGS TO THE CECROPIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995
01-NOV-1995
15-JUN-2002
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EMBL; S74376; AAC60515.1; --
InterPro; IPR000875; Cecropin.
InterPro; IPR003254; IIP_cecropin.
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ProDom; PD003996; IIP_cecropin; 1.
PROSITE; PS00266; CECROPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                   MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
MILE U., Adams M.D., White O., Clayton R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., Tomb J.-F., Dougherty B.A., Merrick J.M., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Gocayne J.D., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Weldman J.F., Phanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YG31_HAEIN
P44279;
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                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; P. Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=727;
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                                                                                                                                                         Science 269:496-512(1995)
                                                                                                                                                                                                                                                                       Venter J.C.;
                                                                                                                                                                                                                                Whole-genome
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(Rel. 32, Last sequence update)
(Rel. 41, Last annotation updat)
1 protein HI1631 precursor.
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AMIDATION (G-62
(BY SIMILARITY)
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BY SIMILARITY.
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                                                                                                                                                                                                                                    and assembly of Haemophilus influenzae
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                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                          -!- SUBUNIT: MONOMER.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CASEIN KINASE I SUBFAMILY.
                                                                                                                                                                                                            "Ovine casein kinase I alpha gene.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR
PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS
AS SUBSTRATES. IT CAN PHOSPHORYLATE A LARGE NUMBER OF PROTEINS.
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

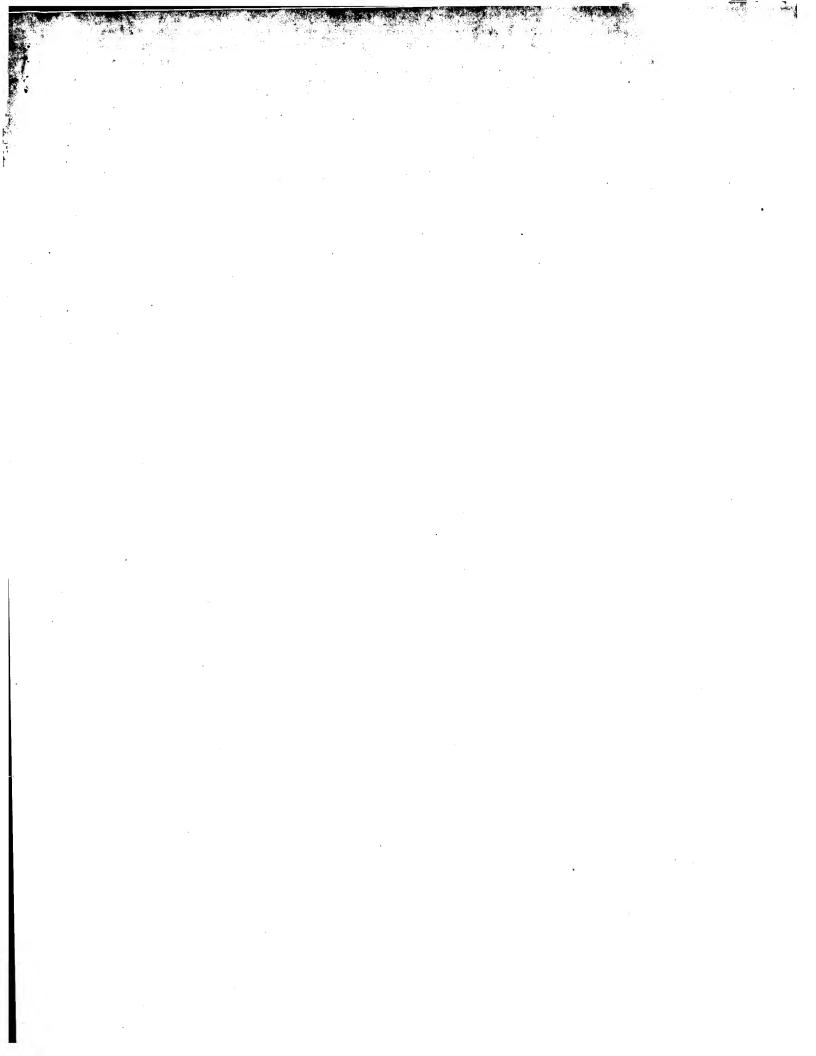
SPECIES=Rabbit; TISSUE=Skeletal muscle;
Zhai L., Depaoli-Roach A.A., Roach P.J.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
SPECIES-BOVINE; TISSUE-Brain;
MEDLINE-92052129; PubMed-1946367;
MEDLINE-92052129; PubMed-1946367;
Rowles J., Slaughter C., Moomaw C., Hsu J., Cobb M.H.;
"Purification of casein kinase I and isolation of cDNAs encoding multiple casein kinase I-like enzymes.";
Proc. Natl. Acad. Sci. U.S.A. 88:9548-9552(1991).
                                                                                                                                                                                                                                                                                                     SPECIES-Sheep; TISSUE-Blood; Yamamoto N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine), Oryctolagus cuniculus (Rabbit), and Ovistolagus cuniculus (Rabbit), and Ovis aries (Sheep).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaila; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Casein kinase I, alpha isoform (EC 2.7.1.-) (CKI-alpha) (CKI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovidae; Bovinae; Bos.
NCBI_TaxID=9913, 9986,
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P35506;
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SIGNAL 1 28 POTENTIAL.
CHAIN 29 190 HYPOTHETICAL PROTEIN HI1631.
SEQUENCE 190 AA; 22314 MW; E4E3ABC7957EC908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entitles requires a or send an email +-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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7; Conserv
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                                  (See http://www.isb-sib.ch/announce/
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                                                                  There are no restrictions ng as its content is in
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EMBL; M76543; AAA30451.1;

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Best Local
                                                                             Multigene family.
DOMANIN 17 2
NP_BIND 23
BINDING 46
ACT_SITE 136
SEQUENCE 325 AA;
                                                                                                                                                                                                                             EMBL;
EMBL;
HSSP;
                                                                                                                                                                           Prodom; PD000001;
PROSITE; PS00107;
                                                                                                                                                                                             InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
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                                                   Local
  16
                                                                                                                                                                                                                                   U59166; AAB03992.1; -. AB050945; BAB17769.1;
                                                                                                                                                                                                                             Q06486; 1CKI
                                         Similarity
8; Conserv
                                                                                                                                                   PS00107; PROTEIN_KINASE_ATP, 1.
PS00108; PROTEIN_KINASE_ST; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
KYKLVRKIGSGSF
                   KWKLFKKIGIGKF 13
                                        Conservative
                                                                                                                                      0011; PROTEIN_KINASE_DOM; 1.
Serine/threonine-protein kinase; ATP-binding;
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                                                                              285 P
31 A
46 A
136 B
136 B
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28
                                                                                       PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                               Score 42; DB 1;
Pred. No. 19;
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Q40166 lycopersico
Q98qc7 mycoplasma
Q9ain5 carsonella
Q9cyl5 mus musculu
Q9u2n8 caenorhabdi
Q8ybf0 brucella me
Q99td7 staphylococ
Q08980 saccharomyc
Q9vn08 drosophila
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Q9uz83 pyrococcus
Q9k5p7 bacillus ha
Q96u53 neurospora
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                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-MB4T / JCM11007;
MEDLINE=21992816; PubMed=11997336;
MEDLINE=21992816; PubMed=11997336;
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., M
Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
EMBL; AE013330; AAM23882.1; -.
                                                                                                                                                                             Complete proteome. SEQUENCE 309 AA;
                                                                                                                                                                                                                                                                                                                                                     Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Bacillus/Clostridium group; (
Thermoanaerobacteriales; Thermoanaerobacteriaceae;
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57 KWKLFPVSGWGTFAHT 172
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01-OCT-2000
01-OCT-2000
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Arginase related (EC 3.5.3.1).
                                                                                                                                                                                        InterPro; IPR003346; Transposase_20.
InterPro; IPR002525; Transposase_9.
Pfam; PF02371; Transposase_20; 1.
Pfam; PF01548; Transposase_9; 1.
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ
EMBL; AJ248287; CAB50176.1;
InterPro; IPR000287; Arginase.
pfam; PF00491; arginase; 1.
PROSITE; PS00148; ARGINASE_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                       "Complete genome sequence of the alkaliphilic halodurans and genomic sequence comparison wit Nucleic Acids Res. 28:4317-4331(2000).

EMBL; APO01520; BAB07760.1;
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MEDLINE=20512582; PubMed=11058132;
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Fuji F., Hirama C., Nakamura Y., O
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Bacillaceae; Bacillus
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Archaea; Euryarchaeota;
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  KWKPFVKRGVGIKRATKLVETAKK
                                      KWKLFKKIGIG----
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427 AA: 49
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                                                                                                                                                         48695 MW;
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                  -KFLHSAKK 19
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                                                                                            Score 47.5;
Pred. No. 18;
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Pred. No. 9
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                                                                                                                                                   proteome.
F7E8099BCDA45C5C
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Ogasawara N.,
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Best Local S
Matches 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              060034;
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SMART; SM00355; ZnF_C2H2; 3.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_2.

DNA-binding; Hypothetical protein; Zinc-finger.

SEQUENCE 501 AA; 56866 MW; 5B7D09A2ED6C90E9
                                EMBL; 268906; CAA93142.1;
InterPro; IPR003593; AAA_
InterPro; IPR003439; ABC_
InterPro; IPR000577; FGGY
                                                                                                                            binding cassette transporters.";
Mol. Gen. Genet. 254:417-426(1997)
                                                                                                                                                                    De Waard M.;
"Multidrug resistance
                                                                                                                                                                                                            Del
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               German Neurospora genome pro
Submitted (NOV-2001) to the
EMBL; AL389890; CAD11797.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Schulte U., Aign V., Nyakatura G., Mewes
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Eukaryota; Fungi; Ascomyco:
Sordariales; Sordariaceae;
                                                                                                                                                                                                                                                                                                        in the plant pathogenic submitted (APR-2000) to
                                                                                                                                                                                                                                                                                                                                            "Characterization
                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SAS56;
                  InterPro;
                                                                                                              -!- SIMILARITY: BELONGS TO
                                                                                                                                                                                                                            MEDLINE-97324590;
                                                                                                                                                                                                                                                  STRAIN-SAS56;
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Similarity 50.0%;
10; Conservative
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                IPR001092;
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                                                                                                                                                                                                                                                                                                      Kan J.A.L., De Waard M.A.;
of a P-glycoprotein-like multi
ogenic fungus Botrytis cinerea.
00) to the EMBL/GenBank/DDBJ da
                                                                                                                                                                                                        PubMed=9180695;
Nistelrooy H.,
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                                                                          AAA_ATPase.
                                  ABC_transportr FGGY_kin.
                  HLH_basic
                                                                                                                                                            in Aspergillus
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Pred. No. 21;
4; Mismatches
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AY072140; AAL59962.1; -
SHAD; AY072140; AAL59962.1; -
SR InterPro; IPR004274; NIF.
SR Pfam; PF03031; NIF; 1.
WHYDOTHELCAL protein.
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Best Local (
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OBVYE2;
OBVYE2;
O1-MAR-2002 (TIEMBLIE1. 20
O1-MAR-2002 (TIEMBLIE1. 20
""N-2002 (TIEMBLIE1. 2)
                                                                                                                                                                  09LG22 PRELIMINARY;
09LG22;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
E14J16.15;
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Best Local
                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eurosids II; Brassicales; Brassicaceae; Arabidopsis.
SEQUENCE FROM N.A.
                                                                                                                                    Arabidopsis thaliana (Mouse-ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
PROSITE; PS00245; FGGY_KINASES_2; UNKNOWN_1.
PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
ATF-binding; Transport.
SEQUENCE 1562 AA; 173535 MW; 89036ECCE3D24919 CRC64;
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nes 8; Conserv
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RESULT 8
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GN GTOM
OS Lyco
OC Euka
OC Speri
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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Q40166;
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ACC02304; ARF9316.1; -.
InterPro; IPRO04274; NIF.
Pfam; PF03031; NIF; 1.
SEQUENCE 414 AA; 46605 MW; 1D21A52D01F8D413 CRC64;
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"Identification and genetic analysis of no:
synthase genes by of tomato by sequencing,
suppression.";
Plant Mol. Biol. 22:589-602(1993).

normal

22:589-602(1993).

MEDLINE-93344508; PubMed-8343597;

SEQUENCE FROM N.A. STRAIN-AILSA CRAIG;

NCBI_TaxID=4081;

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Q98QC7;
01-OCT-2001 (Tremblrel 1
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InterPro; IPR002060; Squ/phyt_synthse.
Iffam; PF00404; SQS_PSY; 1.
PROSITE; PS01044; SQUALEN_PHYTOEN_SYN_1; 1.
PROSITE; PS01045; SQUALEN_PHYTOEN_SYN_2; 1.
SEQUENCE 432 AA; 48775 MW; F609DOCF3272317D CRC64;
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Nucleic Acids Res. 29:2145-2153(2001).
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Moszer I., Dybvig K., Wroblewski H.,
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NCBI_TaxID=2107;
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01-JUN-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Ribosomal protein S19.
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Clark M.A., Baumann L., Thao M.L., Mora "Degenerative Minimalism in the Genome J. Bacteriol. 183:1853-1861(2001). EMBL; AF250389; AAK18640.1; -- HSSP; P80381; 1QKF.
                                                                                                                                                                                                                                                                                                                         Carsonella ruddii.
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79222 MW; D69F28C79661E378 CRC64;
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                                                                                                           Moran N.A., Baumann P.;
nome of a Psyllid Endosymbiont.";
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RA Kawai J., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,
RA Alzawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lawis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lawis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lawis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lawis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Hyons P., Marchionni L., Washima J., Mazzarelli J., Mombaerts P.,
RA Hyons P., Marchionni L., Washima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Redriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local Similarity
Matches 8; Conserv
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Best Local S
Matches 8
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Eukaryota; Metazoa; Mammalia; Eutheria;
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InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
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EMBL; AK017557; BAB30803.1; -.
HSSP; P04284; 1CFE.
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                                                                                                                                                                                                                             SEQUENCE
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Rodentia;
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Pred. No.
                                                                                                                  Score 45; DB 1
Pred. No. 16;
1; Mismatches
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ACCOMPAND ACCOMP
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C STRAIN-16M / ATCC 23456 / BIOTYPE 1;

X MEDLINE-20020109; PubMed-11756688;

AN Delvecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,

RA Ivanova N., Anderson I., Bhattacharryya A., Lykidis A., Reznik G.,

RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

RA Haselkorn R., Kyrpides N., Overbeek R.;

"The genome sequence of the facultative intracellular pathogen

RT Brucella melitensis.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).

DR EMBL; AE009728; AAL54192.1; -.

DR InterPro; IPR001467; Prok_Mboxred.
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Q8YBF0
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Best Local S
Matches 7
               Interpro; IPR00146; Fig. 1.
Pfam; PF00384; molybdopterin; 1.
Pfam; PF01568; Molydop_binding; 1.
PROSITE; PS00490; MOLYBDOPTERIN_PROK_2;
PROSITE; PS00932; MOLYBDOPTERIN_PROK_3;
PROSITE; PS00932; MOLYBDOPTERIN_PROK_3;
           Oxidoreductase;
SEQUENCE 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brucella melitensis.
Bacteria; Proteobacteria;
Brucellaceae; Brucella.
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01-MAR-2002 (TrEMBLrel
01-JUN-2002 (TrEMBLrel
Nitrate reductase alpha
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01-MAY-2000
01-OCT-2001
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Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
NCBI_TaxID=6239;
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EMBL; AL132863; C
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MEDLINE-99069613; PubMed-9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EWKMSKDTKLGKFFH 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KWKLFKKIGIGKFLH 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32863; CAB60572.1;
IPR002900; DUF38.
IPR001810; F-box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) (TrEMBLrel.) (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biology
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        102574 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37863 MW;
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20, La
21, La
chain
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13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oda; Chromadorea; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
in (EC 1.7.99.4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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15278350CB06033F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        925
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35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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Q08900 ID Q0898 AC Q0898 AC Q0898 DT Q1-NO DT Q1-NO DT Q1-VQ Chrom GN YPL26 OS Sacch OC Sacch OC Sacch OC NCBIL RN [1] RP SEQUE RA Deliu RL Submi
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Q99TD7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                               Q08980 PRELIMINARY; 1
Q08980; 01-NOV-1996 (TrEMBLrel. 01, Cr.
01-NOV-1996 (TrEMBLrel. 01, La.
01-JUN-2002 (TrEMBLrel. 21, La.
Chromosome XVI reading frame 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lancet 357:1225-1240(2001).
EMBL; AP003363; BAB57889.1; --
EMBL; AP003134; BAB42816.1; --
EMBL; AP003134; BAB42816.1; --
InterPro; IPR002123; Acyltransferase.
InterPro; IPR004552; AGP_acyltrn.
Pfam; PF01553; Acyltransferase; 1.
TIGRFAMS; TIGR00530; AGP_acyltrn; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 10; Conserv
    SEQUENCE FROM N.A.
Delius H., Hebling U
Submitted (JUN-1996)
                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
                                                                                             Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                       Eukaryota;
                                                                                                                                                                                      YPL264C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q99TD7;
Q99TD7;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Complete proteome.
SEQUENCE 205 AA; 23074 MW; 0078A4DCE66D218E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Whole genome sequencing of meticillin-resistant aureus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Kunamori M., Matsunaru H., Maruyama A., Murakami H., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-J. Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaj Kanehisa M., Yamashita A., Oshima K., Furuya K., Yosi Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315). Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Hypothetical protein SAV1727.
SAV1727 OR SA1548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21311952; PubMed=11418146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus.
NCBI_TaxID=158878,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 55.0
ll; Conservative
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                                                                                                                                          Fungi;
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                                                                                                              Ascomycota; Saccharon; Saccharonycetaceae;
                            u.;
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50.0%;
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Last
e ORF
EMBL/GenBank/DDBJ
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Pred. No.
                                                                                                         Saccharomycotina; Saccl
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Pred. No.
                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                  annotation YPL264C.
                                                                                                                                                                                                                                              sequence
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                                                                                                                                                                                                                                                                                                                353
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1e+02;
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K., Yoshino C.,
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                                                                                                                            Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hosoyama A.,
I., Kaito C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N315);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CO
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databases.

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RN [2]
RD SEQUENCE FROM N.A.
RD Duesterhoeft A., Floeth M., Fritz M., Hilbert H., Moestl D.;
RA Duesterhoeft A., Floeth M., Fritz M., Hilbert H., Moestl D.;
RA Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RL Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP SEDJ SOU06185; YPL264C.
DR InterPro; IPR000620; DUF6.
DR InterPro; IPR000620; DUF6.
DR InterPro; IPR000822; DUF6; 2.
SC SEQUENCE 353 AA; 39702 MW; 68A971BC5DB92988 CRC64;
SEQUENCE 354 AA; 39702 MW; 68A971BC5DB92988 CRC64;
SE
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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 03
Maximum Match 1008
Lasting first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM protein
                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
 seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein search, using sw model
                                                                                                                                                                                                                                                                                                         Query
Match
BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            June 6, 2003, 13:22:41 ; Search time 15.5 Seconds
(without alignments)
133.213 Million cell updates/sec
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108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KWKLFKKIGIGKFLHSAKKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
Cgn2_6/ptodata/2/pubpaa/US09_RUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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- C9n2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep: *
- C9n2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep: *
- C9n2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: *
- C9n2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: *
- C9n2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep: *
- C9n2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep: *
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US-09-904-753-13
US-09-904-753-13
US-09-904-753-13
US-09-908-139-1
US-09-908-139-3
US-09-807-720-3
US-09-807-733-3
US-09-807-733-3
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   Sequence 1, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 211, Appli
Sequence 13, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 121, Appli
Sequence 14, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 110, Appli
Sequence 3, Appli
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US-10-020-079-36	US-10-020-079-18	-10-020-079		US-10-020-079-2	US-10-020-079-4	9-3	US-10-020-079-38		1	10-020-079-	US-10-020-079-6	٠	US-10-020-079-10	US-10-020-079-12	US-10-020-079-14	US-10-020-079-16	US-09-030-619-176	US-09-904-753-5	US-09-371-307-76	US-09-908-139-11	US-09-738-626-6975	US-09-908-139-7	-908-1	-908-139-	US-09-904-753-4
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ALIGNMENTS

RESULT 1 US-10-081-418-1

Sequence 1, Application US/10081418, Publication No. US20030096745A1 GENERAL INFORMATION:

APPLICANT: HAHM, Kyung-Soo
APPLICANT: LEE, Dong Gun
APPLICANT: LEE, Dong Gun
APPLICANT: PARK, YoonKyung
APPLICANT: KIM, Hee Nam
TITLE OF INVENTION: NO. US20030096745A1el peptides with increased + charge
TITLE OF INVENTION: substituting one or more amino acids of CA-MA peptide
TITLE OF INVENTION: pharmaceutical compositions containing thereof
FILE REFERENCE: 428.1014

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CURRENT APPLICATION NUMBER: US/10/081/418

CURRENT FILING DATE: 2002-02-22

INUMBER OF SEQ ID NOS: 2

SOFTWARE: Kopatentin 1.71

SEQ ID NO 1

LENGTH: 20

TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OFFER INFORMATION: CA-MA peptide made by fusing 1-8 amino acid of secropin A and US-10-081-418-1

US-10-081-418-1

Ouery Match
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OWNER INFORMATION: 1-12 amino acid of magainin 2

OUERY MATCH
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OWNER INFORMATION: 1-12 amino acid of magainin 2

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Sequence 7, Application US/09820053A

Publication No. US20030083243A1

GENERAL INFORMATION:
GENERAL INFORMATION:
FILE REFERENCE: HELXO27

FILE REFERENCE: HELXO27

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 165

SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: antimicrobial cationic peptide
US-09-908-139-6
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US-09-820-053A-7
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                                                                                                                                                                                RESULT 4
US-09-904-753-2
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CURRENT APPLICATION NUMBER: US/09/908,139
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/143,124
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 32
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                                                                                                     Sequence 2, Application US/09904753
Publication No. US20030092612A1
GENERAL INFORMATION:
APPLICANT: Lynos, Robert T
                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                               Query Match
TITLE OF INVENTION: Use of ANtimicrobal Peptides as Preservatives in TITLE OF INVENTION: Ophthalmic Preparations, Including Solutions, TITLE OF INVENTION: Emulsions, and Suspentions FILE REFERENCE: 2973 ver 2
CURRENT APPLICATION NUMBER: US/09/904,753
CURRENT FILING DATE: 2001-07-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
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OTHER INFORMATION: SYNTHETIC SEQUENCE
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Local Similarity 72.2%;
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12; Conservative
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Woods, Donald
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                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                Score 63;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-030-619-211
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US-09-904-753-13
; Sequence 13, Application US/09904753
; Publication No. US20030092612A1
; GENERAL INFORMATION:
; APPLICANT: Lynos, Robert T
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SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
LENGTH: 23
                         PRIOR APPLICATION NUMBER: WO 96/25183
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 14
SOSTWARE: PATENTIN Ver. 2.1
SEQ ID NO 13
LENGTH: 26
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Best Local
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LENGTH: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MCNICOL, PATRICIA J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE
TITLE OF INVENTION: WITH ANTIBIOTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                            CURRENT APPLICATION NUMBER: US/09/904,753 CURRENT FILING DATE: 2001-07-13
                                                                                                                                                          TITLE OF INVENTION: Use of ANTIMIC Preparations, Including Solutions, TITLE OF INVENTION: Emulsions, and Suspentions
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TYPE: PRT
TYPE: PRT ORGANISM: Artificial Sequence
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Erfle, Douglas
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; Pred. No. 0.0018;
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pred. No.
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APPLICANT: HANCOCK, Robert E. W.
APPLICANT: Gough, Monisha A.
APPLICANT: Gough, Monisha A.
APPLICANT: Gough, Monisha A.
APPLICANT: Batrzykat, Aleksander
APPLICANT: Woods, Donald
APPLICANT: Jia, Xiaoyan
TITLE OF INVENTION: APTI-ENDOTOXIC, ANTIMICRUTILE OF INVENTION: PEPTIDES AND METHODS OF
FILE REFERENCE: 07422/016001
CURRENT APPLICATION NUMBER: US/09/908,139
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/143,124
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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; OTHER INFORMATION:
US-09-904-753-13
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                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09908139 Publication No. US20030096949A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 120
LENGTH: 26
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Best Local Similarity
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
TITLE OF INVENTION: WITH ANTIBIOTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE:
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APPLICANT: Krieger
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les 12; Conserv
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Erfle, Douglas
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Description of Artificial Sequen
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85.7%;
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85.7%;
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Pred. No. 0.
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Pred. No. 0.002;
0; Mismatches
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                                                                                                                                                   ANTIMICROBIAL CATIONIC ETHODS OF USE THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
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CURRENT APPLICATION NUMBER: US/09/030,619B; CURRENT FILING DATE: 1998-02-25; SOFTWARE: Fastsed for Windows Version 3.0; SEQ ID NO 121; LENGTH: 28; TYPE: PRT
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LENGTH: 28
TYPE: PRT
                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                           GENERAL
                                                                                                         TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALC FILE OF INVENTION: WITH ANTIBIOTICS FILE REFERENCE: 660081.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                       Patent No. US20020035061A1
                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/909,652
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/219,179
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bylina, Edward J.
APPLICANT: Coleman, William J.
APPLICANT: Youvan, Douglas C.
TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR GENERATING
TITLE OF INVENTION: AND SCREENING COMPOUNDS THAT AFFECT CI
FILE REFERENCE: 22346-7001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kairos Scientific, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: CEMA analogue of cecropin-melittin hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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                                                                                                                                                                                      Taylor, Robert
Erfle, Douglas
Fraser, Janet R.
West, Michael H.P.
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12; Conser
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                                                                                                                                                                                                                                                        Krieger, Timothy J.
                                                                                                                                                                                                                                                                                                      Application US/09030619B
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85.7%;
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85.7%;
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Pred. No.
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Pred. No.
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0.0022;
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; OTHER INFORMATION: Cationic Peptide Analogue US-09-030-619-121

ORGANISM: Artificial Sequence FEATURE:

Matches

12;

Conservative

0

Mismatches

Query Match Best Local Similarity

58.3%;

Score 63; DB 10; Pred. No. 0.0022;

Length 28;

Indels

0;

Gaps

0;

0;

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GENERAL INFORMATION:
APPLICANT: OWED, Donald R.
FILE OF INVENTION: SHORT BIOACTIVE PEPTIDES
FILE REFERENCE: HELX027
CURRENT APPLICATION NUMBER: US/09/820,053A
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 165
SOOTWARE: Patentin Ver. 2.1
SEQ ID NO 146
LENGTH: 23
TYPE: PR
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; TYPE: PRT
; ORGANISM: Xenopus laevis
US-09-917-340-4
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                                   ; OTHER INFORMATION: AMIDATION US-09-820-053A-146
                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-820-053A-146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Transplant Media FILE REFERENCE: TPLANT-06468 CURRENT APPLICATION NUMBER: US/09/917,3 CURRENT FILANG DATE: 2001-07-29 PRIOR APPLICATION NUMBER: 60/221,632 PRIOR APPLICATION NUMBER: 60/249,602 PRIOR FILING DATE: 2000-07-28 PRIOR FILING DATE: 2000-11-17 PRIOR FILING DATE: 2000-11-17 PRIOR FILING DATE: 2000-11-17
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Query Match
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PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: McAnulty, Jos
APPLICANT: Reid, Ted W.
                                                                        NAME/KEY: MOD_RES
                                                                                                              OTHER INFORMATION: SYNTHETIC SEQUENCE:
                                                                                                                               FEATURE:
                                                                                                                                                 ORGANISM: ARTIFICIAL SEQUENCE
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ty, Jonathan F.
     55.6%;
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     Score 60;
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0.024;
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     9;
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   Length 23;
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US-09-908-139-9
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APPLICANT: Lynos, R
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SEQ ID NO 9
                                                                                                                             LENGTH: 23
TYPE: PRT
ORGANISM: Xenopus laevis
PUBLICATION INFORMATION:
AUTHORS: Lee et al.,
                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local S
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TITLE OF INVENTION: ANTI-ENDOTOXIC, ANTIMICROBIAL CATIONIC
TITLE OF INVENTION: PEPTIDES AND METHODS OF USE THEREFOR
FILE REFERENCE: 07422/016001
CURRENT APPLICATION NUMBER: US/09/908,139
CURRENT FILING DATE: 2001-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09904753 Publication No. US20030092612A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/143,124
PRIOR FILING DATE: 1998-08-28
NUMBER OF CENTER 1998-08-28
                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Use of ANtimicrobal Peptides as Preservatives in TITLE OF INVENTION: Ophthalmic Preparations, Including Solutions, TITLE OF INVENTION: Emulsions, and Suspentions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hancock, Robert E. W. APPLICANT: Gough, Monisha A.
                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/904,753
CURRENT FILING DATE: 2001-07-13
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                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: WO 96/25183
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 14
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                                                                      TITLE: High-Level Expression of Antimicrobal Peptide Mediated TITLE: by a Fusion Partner Reinforcing Formation of Inclusion TITLE: Bodies
PAGES: 575-580
DATE: Sept 21, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 33
                                   JOURNAL: Biochem. Biophys. Res. Commun VOLUME: 277
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12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.6%;
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1; Mismatches
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Pred. No. 0.
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US-09-904-753-1

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APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Taylor, Robert
APPLICANT: Erfle, Douglas
APPLICANT: Erfle, Douglas
APPLICANT: Fraser, Janet R.
APPLICANT: Fraser, Janet R.
APPLICANT: Mest, Michael H.P.
APPLICANT: Mest, Michael H.P.
APPLICANT: Mest, Michael H.P.
APPLICANT: Mest, Michael H.P.
APPLICANT: MICHAEL H.P.
APPLICANT: MICHAEL J.
APPLICATION UNIMER: US/09/030,619B
CURRENT FILING DATE: 1998-02-25
CURRENT FILING DATE: 1998-02-25
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 210
SEQ ID NO 210
LENGTH: 23
TYPE: PRT
ORGANISM: Xenopus laevis
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Search completed: June 6, 2003, 13:26:02 Job time: 15.5 secs
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Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                    9 GIGKFLHSAKKF 20
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1 GIGKFLHSAGKF 12
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1 GIGKFLHSAGKF 12
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                                                                                                                                                                    Score 56; DB 10; Length 23; Pred. No. 0.024; 1; Indels
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS	AAR45136	AAR21402	AAG47538	AAG47565	AAG22998	AAG47539	AAG47540	AAG47566	AAG22999	AAG47567	AAG23000	AAB50847	AAW71679	AAR22835	AAR21351	AAE22455	AAY10742	AAW66488	AAR90251	AAR59057	AAR56940	AAR50555	AAR50440	AAR55979	AAR35373	AAR31155	AAR33965	AAR45124	AAR22844	AAR21361	AAR21360	AAR22869	AAR21385	65	AAR84924
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Feige U, Liu C, Cheetham J, Boone TC;		(AMGE-) AMGEN INC.			23-OCT-1998; 98US-0105371.		25-OCT-1999; 99WO-US25044.		04 - MAY - 2000.		WO200024782-A2.		Synthetic.	•	asthma; thrombosis; pharmaceutical.	vascular endothelial growth factor; matrix metalloproteinase;	cytotoxic T cell lymphocyte antiqen 4: tumour necrosis factor:	MMP; inhibitor; erythropoietin; thrombopoietin; interlenkin 1;	immunosuppressive; EPO; TPO; CTLA4; mimetic: IL-1: TNF: antagonist.	autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF:	Modified peptide; therapeutic agent; fusion: Fc domain: cancer:		Calmodulin antagonist peptide sequence SEO ID NO.179		31-OCT-2000 (first entry)		AAB17123;		AAB17123 standard; Peptide; 18 AA.	AAB17123	ULT 1

Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating cancer and

autoimmune diseases

2000-350702/30

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RESULT 2
ABB73201
ID ABB7
XX ABB7
AC ABB7
XX Modi
KW EPO;
KW TNF
KW TPO
KW TPO
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KW AMP
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(X)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each

(I)c-P1-(L2)d-P2.

(L1)c-P1-(L2)d-P2.

(L1)c-P1-(L2)d-P2.

(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4

(Where P1, P2, P3, and P4 = are each independently sequences of

pharmacologically active peptides; I1, L2, L3, and L4 = are each

(C) or I, provided that at least 1 of a and b is 1. The composition can

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Matches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor; TMF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP; TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist; MMP inhibitor; antiinflammatory; antiitumour; immunosuppressive; cytostatic; antirheumatic; antiiarthrikic; antidiabetic; ophthalmological; neuroprotective; inflammatory disease; autoimmune disease; tumour growth; cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity; sleep disorder; neurological degenerative disease; are themewish perioder in the second of the second content of the second co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Calmodulin antagonist peptide SEQ ID NO:179.
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Synthetic.
                                                                                                     03-MAY-2000; 2000US-0563286
                                                                                                                                                                                                          02-MAY-2001; 2001WO-US14310
                                                                                                                                                                                                                                                                                                               08-NOV-2001
          (AMGE-) AMGEN
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Sequence

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Length 18;

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cc The present invention describes a vehicle-peptide molecule (I) or its cytostatic, antirheumatic, antiaritaritaritic, antidiabetic, ophthalmological, cortostatic, antirheumatic, antidiabetic, ophthalmological, cantianaemic, anorectic, antiinfertility, haemostatic, dermatological, cc antianaemic, anorectic, antiinfertility, haemostatic, dermatological and cc prophylactic agent as well as for screening purposes. (I) is useful for cd diagnosting diseases characterised by dysfunction of their associated cc protein of interest, for identifying normal or abnormal proteins of interest, as a part of diagnostic kit to detect the presence of their creating of interest in a biological sample. Additionally, (I) is useful creating of interest in a biological sample additionally, (I) is useful creating of interest in a biological sample. Additionally, (I) is useful cortinated architity, and neurological degenerative diseases, tumour growth, cancer, creatinity, and neurological degenerative diseases. (I), comprising cc ponimetic compounds are useful for treating disorders characterised by compounds are useful for treating conditions that involve an existing cc megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet cc cmegakaryocyte/platelet acid seguences used in the represent amino acid and nucleic acid sequences used in the
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                                               exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   retinopathy, obesity, sleep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 53; 176pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cheetham
                                               the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ule or its multimers useful for treating diseases, cancer, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders and infertility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TC,
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RESULT 3
AAR21399
AC XXX DEE CONTRACTOR OF CONTR
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence of amphiphilic peptide SEQ ID No. acetylated N-terminus, may be a C-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amphiphilic spermicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAY-1992
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                                                                                                                                                                                                                                                  19-JUL-1990;
                                                                                                                                                                                                                                                                                                                      17-JUL-1991;
                                                                                                                                                                              (SCRI-) SCRIPPS RES INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide; anti-microbial; anti-viral; anti-tumour;
wound healing; sterilant.
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                                                                                                      Blondelle
                                                                                                                                                                                                                                                      90US-0554422
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Pred. No. 0.
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WPI; 1992-064700/08

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RESULT 4
AAR22883
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Best Local :
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The amphiphilic peptide (SEQ ID NO 62) was prepd. by standard solid phase methods. The peptide is an analogue of the peptide having SEQ ID NO 3 (AAR22824), with an N-terminal extension of 1 amino acids. Substitution and deletion analogues of this peptic
                                                                                                                                   Claim
                                                                                                                                                                                          Amphiphilic peptide(s) and analogues - i
                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                               08-JUL-1991;
19-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial; antiparasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The peptides of the invention are effective pharmaceuticals having anti-microbial, anti-viral and anti-tumour activity. They are also useful for inhibiting, preventing or destroying the motility of sperm and hence have application in a spermicide preparation. They also have anti-parasitic activity and are useful in wound healing, as preservatives and sterilants and to inhibit growth of phytopathogenic microorganisms. AAR20969 and AAR20970 were published in Halghten and Ostresh, Bio Chromatography, Vol 2, issue 2, page 80-83, 1007
                                                                                                                                                                                                                                                                                                                        Houghten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JAN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 60;
                                                                                                                                                                                                                                                                       1992-114943/15.
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                                                                                                                              60;
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90US-0554442.
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spermicides; burns; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91CA-2024317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "amidated"
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                                                                                                                                                                                                                     for use in
                                                                                                                                                                                               compositions,
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peptide
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RESULT 5
AAR21400
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Best Local :
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                                                                                                                                                     anti-microbial, anti-viral and anti-tumour activity. They are also useful for inhibiting, preventing or destroying the motility of sperm and hence have application in a spermicide preparation. They also have anti-parasitic activity and are useful in wound healing, as preservatives and sterilants and to inhibit growth of phytopathogenic microorganisms. AAR20959 and AAR20970 were publish the property of the prope
                                                                                           Sequence
                                                                                                                                                                                                                                                                                                   The peptides of the invention are effective pharmaceuticals having
                                                                                                                                                                                                                                                                                                                                                                                              Method for inhibiting target cell and virus growth - administering amphiphilic peptide compsns, useful for viral and phytopathogenic infections, tumours and but
                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 61; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houghten RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUL-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                have increased biological activity and are effective as pharm ceuticals e.g. antibiotics for bacterial, fungal or viral infections, or in spermicides or antinuour or antiparasitic agents. Additionally the peptides can be used in wound healin compans. or for treating burns or other skin or eye infection can also antopological purpose or other skin or eye infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SCRI-) SCRIPPS RES INST.
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16; Conserv
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wound hea
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N-terminus, may be a
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                     61.0%;
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80.0%;
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                                                                                                                                                Chromatography,
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Score 64; DB
Pred. No. 0.14
0; Mismatches
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Pred. No.
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C-terminal
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1.14;
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                                                                                                                                                   AAR20970 were published 2, issue 2, page 80-83,
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or treating
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RESULT 6
AAR22484
ID AAR27
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XX AAR27
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XX O8---
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TAX O8---
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RESULT 7
AAR21398
ID AAR2
XX
AC AAR2
XC AAR2
XX
DT 16-P
XX
XX
DE Sequ
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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The amphiphilic peptide (SEQ ID NO 63) was prepd. by standard solid phase methods. The peptide is an analogue of the peptide having SEQ ID NO 3 (AAR22824), with an N-terminal extension of 18 amino acids. Substitution and deletion analogues of this peptide have increased biological activity and are effective as pharmaceuticals e.g. antibiotics for bacterial, fingal or viral infections, or in spermicides or antitumour or antiparasitic agents. Additionally the peptides can be used in wound healing compsns. or for treating burns or other skin or eye infections. See also AAR22822-89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amphiphilic
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19-JUL-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amphiphilic peptide(s) and analogues - i antimicrobial, antifungal or antitumour increased biological activity
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                                                                                                  AAR21398
  Sequence of
                                               16-MAY-1992
                                                                                                                                                  AAR21398 standard; peptide;
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  amphiphilic peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antifungal; antitumour; pharmaceuticals; antibiotics;
spermicides; burns; wound healing.
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90US-0554442.
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36
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                                                                                                                                                  26
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Pred. No. 0.14
0; Mismatches
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       SEQ
       ID No.
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0.14;
       61 with
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RESULT 8
AAR22882
ID AAR2
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The peptides of the invention are effective pharmaceuticals having anti-microbial, anti-viral and anti-tumour activity. They are also useful for inhibiting, preventing or destroying the motility of sperm and hence have application in a spermicide preparation. They also have anti-parasitic activity and are useful in wound healing, as preservatives and sterilants and to inhibit growth of phytopathogenic microorganisms. AAR20969 and AAR20970 were publish that property and account of the phytopathogenic microorganisms. AAR20969 and AAR20970 were published that the property of the phytopathogenic microorganisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Method for inhibiting target cell and virus growth - comprises administering amphiphilic peptide compsns, useful for treating viral and phytopathogenic infections, tumours and burns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amphiphilic peptide; anti-microbial; anti-viral; anti-tumour; spermicide; wound healing; sterilant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acetylated N-terminus, may be a C-terminal amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haighten
1987.
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                                                                                                                                                                                                                                                                                   AAR22882 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                         CA2047317-A.
                                                                                            Modified-site
                                                                                                                   Key
Modified-site
                                                                                                                                                      Synthetic
                                                                                                                                                                            antiparasitic;
                                                                                                                                                                                          Antimicrobial;
                                                                                                                                                                                                              Amphiphilic peptide
                                                                                                                                                                                                                                       22-AUG-1992
                                                                                                                                                                                                                                                              AAR22882;
           18-JUL-1991;
                                   20-JAN-1992.
                                                                                                                                                                                                                                                                                                                                                             3 KKLLKKPPPLLKKLLKKL
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15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         26
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                                                                                                                                                                            antifungal; antitumour;
spermicides; burns; woun
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           91CA-2024317.
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                                                                                  /note= "amidated"
                                                                                                       note=
                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                    Peptide;
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72pp; English.
                                                                                                         "acylated"
                                                                                                                                                                                                               inhibit growth of a target cell.
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                                                                                                                                                                                                                                                                                                                                                                                              0;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                               our; pharmaceuticals; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                          DB 13;
0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR20970 were published
2, issue 2, page 80-83,
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                                                                                                                                                                                             antibiotics;
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RESULT 9
AARS 5057
ID AARS
XX AARS
XX AARS
XX 17-M
XX 19-M
XX Sept
KW gram
KW poly
XX 10ng
XX 901
XX 901
XX 06-D
XX 06-D
XX 07-C
XX WPI;
PR 07-C
XX WPI;
PR WPI;
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XX WPI;
XX WPI;
XX D1sc
XX D1sc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       solid phase methods. The peptide is an analogue of the peptide having SEQ ID NO 3 (AAR22824), with an N-terminal extension of 8 amino acids. Substitution and deletion analogues of this peptide have increased biological activity and are effective as pharmaceuticals e.g. antibiotics for bacterial, fungal or viral infections, or in spermicides or antitumour or antiparasitic agents. Additionally the peptides can be used in wound healing compans. or for treating burns or other skin or eye infections.
       Disclosure; Page 120; 141pp; English
                              New conjugates of bioactive amphiphilic peptide(s) moiety - are useful for treatment of septic shock
                                                                                                                          (MAGA-)
                                                                                                                                                 07-DEC-1992;
                                                                                                                                                                         06-DEC-1993;
                                                                                                                                                                                                 23-JUN-1994
                                                                                                                                                                                                                        W09413697-A
                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                     septic shock; bacterial endotoxin; lipopolysaccharide; LPS; gram negative bacteria; conjugate molety; septicemia; neutralising; longer activity; polyvinylpyrrolidone; dextran; hetastarch; polyvinyl alcohol; ion-channel forming: amphinhilic
                                                                                                                                                                                                                                                                                                                                                             17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                      AAR56957;
                                                                                                                                                                                                                                                                                                                                 Peptide which neutralises bacterial endotoxin
                                                                                                                                                                                                                                                                                                                                                                                                            AAR56957 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 30; Page 60; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amphiphilic peptide(s) and analogues - antimicrobial, antifungal or antitumous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            increased biological activity
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19-JUL-1990;
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                                                                                                                      MAGAININ PHARM INC
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15; Conserv
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                                                                                                                                               92US-0987443
                                                                                                                                                                        93WO-US11841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ptide(s) and analogues - for use in e.g.
antifungal or antitumour compositions, having
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90US-0554442.
                                                                                               Williams TJ
                                                                                                                                                                                                                                                                                                                                                                                                            peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19
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Pred. No.
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RESULT 10
ABB74249
ID ABB74
XX ABB74
AC ABB74
XX I8-AP
AC ABB74
XX I18-AP
AC ABB74
XX I18-AP
AC ABB74
XX I18-AP
AC ABB74
XX I19-OS
KW Fusog
KW I19-OS
KW PPH
WO200
XX Synth
XX Synth
XX Synth
XX WO200
DD 13-DE
AC O8-JU
AC OS
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Best Local
The present invention describes a method for producing micelles with entrapped therapeutic agents. The method comprises: (1) combining negatively charged agent with a cationic lipid in a ratio where 30-90 % of the negatively charged atoms are neutralised by positive charges on lipid molecules to form an electrostatic micelle complex in 20-80 % ethanol; and (2) combining the micelle complex of (a) with fusogenic-karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing micelles with entrapped therapeutic agents. Also described is a method for delivering a therapeutic agent in vivo, comprising the administration of the micelle. ABB74256 to ABB74858 represent specifically claimed nuclear localisation signal (NLS) peptides for use in the method as the fusogenic-karyophilic peptides. The micelles produced can have cytostatic and antitumour activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Encapsulation of plasmid DNA (Lipogenes) and therapeutic agents with nuclear localization signal/fusogenic peptide conjugates into targets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-164295/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Septic shock is often due to the body's reaction to foreign lipopolysaccharide (LPS). The compounds of the invention neutralise bacterial endotoxins without neutralising essential proteins in the plasma of patients, eg.heparins. They also have longer duration of activity than unconjugated peptides. In general peptides such as this are ion-channel forming peptides. The compounds are biologically active peptides ilnked to a conjugate moiety, eg. carbohydrates, proteins, polyvinylpyrrolidone, polyalkylene glycols and polyvinyl alcohols. The conjugate moiety may be linked at the C- or N-terminal or internally of the peptide. AARS5591-631 and AARS56879-957 are examples
                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Page 38; 107pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JUN-2000; 2000US-210925P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUN-2001; 2001WO-US18657.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene; liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour; peptide-lipid-polynucleotide complex; neoplastic disease; gene therap breast carcinoma; prostate carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-DEC-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liposome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BOUL/) BOULIKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amphiphilic fusogenic peptide SEQ ID NO:15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB74249;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Region
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                                                                                                                                               The present peptide is a specific example of a cationic oligopeptide corresp. to the formula (b-l-1-b)n, where b is a hydrophobic amino acid, lis a hydrophilic amino acid and n is at least 4. In this case, where b is Leu, l is Lys and n = 10, the oligopeptide forms an alpha-helix which forms a stable complex with a nucleic acid. The complex is suitable for transferring nucleic acid, esp. in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                            Complex of nucleic acid and oligopeptide with sec. structure transfer vectors contg. them, useful for efficient transfer of nucleic acid to cells in gene therapy.
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                                                                                                                                                                                                                                                                                                                               Claim 6 and
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83.3%;
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                                                                                                                                                                                                                                                                                                                                    Page 7; 20pp;
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14-MAY-1990;
28-APR-1992;
17-NOV-1994;
                                                                                   The invention relates to analogues of a magainin I or II, D-form analogues, deletion analogues or related peptides. It also relates to basic polypeptides having at least 16 amino acids, including at 18 hydrophobic amino acids and at least 8 hydrophilic amino acids. The peptides may be used as antimicrobial agents, antiviral agents, antiviral agents, preservatives or sterilants, or agents for promoting wound healing. present sequence represents a specific example of a peptide disclose the specification.
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                                                                     Sequence
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                                    Conservative
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90US-0476629.
90US-0522688.
92US-0874685.
94US-0343882.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   antimicrobial; antitumour; wound healing;
                                           52.4%;
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                                                                                                               Synthetic.
                                                                                                                                      Antimicrobial; antiparasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                               The peptides of the invention are effective pharmaceuticals having anti-microbial, anti-viral and anti-tumour activity. They are also useful for inhibiting, preventing or destroying the motility of sperm and hence have application in a spermicide preparation. They also have anti-parasitic activity and are useful in wound healing, as preservatives and sterilants and to inhibit growth of phytopathogenic microorganisms. ARR20969 and ARR20970 were published Halghten and Ostresh, Bio Chromatography, Vol 2, issue 2, page 80-83, 1087
                                                Modified-site
                                                                        Modified-site
                                                                                                                                                                     Amphiphilic peptide to inhibit growth of a target cell.
                                                                                                                                                                                                     22-AUG-1992
                                                                                                                                                                                                                                                   AAR22869 standard; Peptide;
                                                                                                                                                                                                                              AAR22869
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAY-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                    17 AA;
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                                             /note-
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     Method for inhibiting target cell and virus growth -administering amphiphilic peptide compsns, useful for viral and phytopathogenic infections, tumours and bur
                                                                                                                                                                                                     Amphiphilic peptide; anti-microbial; spermicide; wound healing; sterilant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The amphiphilic peptide (SEQ ID NO 48) was prepd. by standard solid phase methods. The peptide is an analogue of the peptide having SEQ ID NO 3 (AAR22824), with Leu at position 4 deleted. Substitution and deletion analogues of this peptide have increased biological activity and are effective as pharmaceuticals e.g. antibiotics for bacterial, fungal or viral infections, or in spermicides or antitumour or antiparasitic agents. Additionally the peptides can be used in wound healing compsns. or for treating burns or other skin or eye infections.
                                                      WPI; 1992-064700/08.
                                                                                                                    19-JUL-1990;
                                                                                                                                                                06-FEB-1992
                                                                                                                                         17-JUL-1991;
                                                                                                                                                                                    WO9201462-A
                                                                                                                                                                                                                                   Sequence of amphiphilic peptide SEQ ID Nerminal amide and/or may be acetylated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 54; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amphiphilic peptide(s) and analogues - for use in e.g. antimicrobial, antifungal or antitumour compositions, having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   increased biological activity
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19-JUL-1990;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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(without alignments)
153.815 Million cell updates/sec
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$\text{A}$ \text{A}$ \text
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Query Match Best Local Similarity

47.6%;

Score 50; pred. No.

DB 2;

Length 900;

RESULT 2 T47732 T47732 probable translation initiation factor eIF-3 chain 8 F18021.110 [imported] C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-May-2000 C;Accession: T47732 R;Benes, V; Wurmbach, E; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Rudd, S.; submitted to the Protein Sequence Database, April 2000 A;Reference number: Z24474 A;Accession: T47732 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-900 <ben> A;Cross-references: EMBL:ATF18021 A;Experimental source: cultivar Columbia; BAC clone F18021 C;Genetics: A;Map position: 3 A;Introns: 8/3; 593/3 A;Note: F18021.110</ben>	RESULT 1 T24797 hypothetical protein T10C6.7 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Accession: T24797 R; McMurray, A. submitted to the EMBL Data Library, March 1997 A; Reference number: Z1936 A; Accession: T24797 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Cross-references: EMBL: Z93388; PIDN:CAB07663.1; GSPDB:GN00023; CESP:T10C6.7 A; Cross-references: EMBL: Z93388; PIDN:CAB07663.1; GSPDB:GN00023; CESP:T10C6.7 A; Genetice: A; Genet	30 44.5 42.4 629 2 A71023 31 44 41.9 91 2 T08131 32 44 41.9 143 2 T09232 33 44 41.9 143 2 T09232 34 41.9 146 2 T45838 34 41.9 224 2 F96668 35 44 41.9 319 2 S34806 36 44 41.9 319 2 S34806 37 44 41.9 469 2 JC5798 39 44 41.9 681 2 C84612 40 44 41.9 779 2 S56245 41 44 41.9 781 2 JC7382 42 41.9 893 2 JC7382 43 41.9 893 2 JC7382 44 41.9 1073 1 T08228 45 44 41.9 1309 1 S35484 46 41.9 1309 1 S35484 ALIGNNENTS
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A;Title: The genome sequence of the A;Reference number: A81250; MUID:201 A;Accession: E81331
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A; Cross-references: GB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: dsDNA virus
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 12-Nov-1999
C;Accession: D72863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AcOrf-107 protein - Autographa californica nuclear polyhedrosis virus C; Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
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A;Residues: 1-900 <KAR>
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T50773
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                                                                                                                                                                                                                                                                                                 46.78;
64.78;
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                              e of the food-borne pathogen Campylobacter jejuni reveals MUID:20150912; PMID:10688204
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Pred. No.
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                                                                                     Chilli
                                                                      Barre.
                                          hу
                                          B
                                                                   δã
                                                                                                                                              A; Molecule type; mRNA
A; Residues: 1-1235 <DAV>
A; Cross-references: EMBL: X60421; NID: 91657;
C; Keywords: liver; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                             RESULT 7
S24109
RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                             QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: SGD:PUF6; MIPS:YDR496c
A;Cross-references: SGD:S0002904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-656 <DIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                               Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession:
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C;Superfamily: uroporphyri
C;Keywords: carbon-carbon
                                                                                               Matches
                                                                                                                            Query Match
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A; Residues: 1-340 <PAR>
A; Cross-references: GB: AL139077;
                                                                                                                                                                                                             Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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Best Local Similarity
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                                    734 LVDSPQPLLKRILKRL
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                                                                                                Similarity
9; Conserv
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                                                              LLKKPPPLLKKLLKKL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                WERLRVKTPPLPKQIREKL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S69554
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                                                                                                         46.78;
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47.48;
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55.0%;
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                                                                                                      Score 49;
Pred. No.
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Pred. No.
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R;Davidson, J.J.; Dezcelik, T.; Hamacher, C.; Willems, P.J.; Francke, U.; Kilimann, M. Proc. Natl. Acad. Sci. U.S.A. 89, 2096-2100, 1992
A;Title: cDNA cloning of a liver isoform of the phosphorylase kinase alpha subunit an A;Reference number: S24109; MUID:92196064; PMID:1372435
A;Accession: S24109
                                                                                                                                                                                                                                                                             phosphorylase kinase (EC 2.7.1.38) alpha chain, hepatic - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999 C;Accession: S24109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, August 1995
A;Description: The sequence of S. cerevisiae cosmids 8166, 9787,
A;Reference number: S69553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U33057; NID:g927764; PID:g927766; GSPDB:GN00004; MIPS:YDR496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein YDR496c - yeast (Saccharomyces C;Species: Saccharomyces cerevisiae C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uroporphyrinogen decarboxylase
cbon-carbon lyase; carboxy-lyase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 49; DB
Pred. No. 19;
        Mismatches
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                       DB
71;
                                                                                                   PIDN:CAA42952.1; PID:g1658
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37;
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                                          Length 1235;
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      Indels
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Gaps
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A.Description: catalyzes the hydolysis of peptides A;Note: cleaves preferentially after tyrosine, methionine, or arginine residues and befc C;Superfamily: calpain large chain; calmodulin repeat homology; calpain catalytic domain C;Seywords: acetylated amino end; calcium binding; cysteine proteinase; EF hand; heterod F;2-700/Product: calpain large chain 2 #status predicted <MAT>
                                                                                                                                                                                                                       F;2-700/Product: calpain large chain 2 status prec
F;75-327/Domain: calpain catalytic domain homology
F;529-560/Domain: calmodulin recent homology
                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:119750; OMIM:114230
A;Map position: lpter-lqter
C;Complex: heterodimer of L (large) and S (small) chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA; protein
A;Residues: 1-210,'I','212-394,'D',396-445,'I',447-700 <IMA>
A;Residues: 1-210,'I','212-394,'D',396-445,'I',447-700 <IMA>
A;Cross-references: GB:M23254; NID:g511636; PIDN:AAA35645.1; PID:g511637
A;Note: parts of this sequence were determined by protein sequencing; the R;Hata, A.; Ohno, S.; Akita, Y.; Suzuki, K.

J. Biol. Chem. 264, 6404-6411, 1989
A;Title: Tandemly reiterated negative enhancer-like elements regulate tran A;Reference number: A33529; MUID:89197947; PMID:2539381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Molecule type: mRNA
A:Residues: 1-700 <SOR>
R:Imajoh, S.; Aoki, K.; Ohno, S.; Emori, Y.; Kawasaki, H.; Sugihara, H.; Suzuki, K.
Biochemistry 27, 8122-8128, 1988
A:Title: Molecular cloning of the cDNA for the large subunit of the high-Ca(2+)-requiring A:Reference number: A31218; MUID:89166474; PMID:2852952
A;Accession: A31218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-67,'G',69-72,'IE',75-78,'R' <HAT>
A;Cross references: DDBJ:J04700; NID:g179910; PIDN:AAA52760.1; PID:g463086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Sorimachi, H.; Ohmi, S.; Emori, Y.; Kawasaki, H.; Saido, T.C.; Ohno, S.; Biol. Chem. Hoppe-Seyler 371(Suppl.), 171-176, 1990
A;Title: A novel member of the calcium-dependent cysteine protease family.
A;Reference number: S10589; MUID:90380278; PMID:2400579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Species: Homo sapiens (man)
C:Date: 21-Nov-1993 #sequence_revision 09-Aug-1997 #text_change 16-Jul-1999
C:Accession: S10590; A31218; A33529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Calpain (EC 3.4.22.17) large chain 2 - human
N:Alternate names: calpain chain L-2; calpai
                                               ;529-560/Domain: calmodulin repeat homology <EFT>;572-604/Domain: calmodulin repeat homology <EFT2>;605-634/Domain: calmodulin repeat homology <EFT2>;605-634/Domain: calmodulin repeat homology <EFT3>;637-669/Domain: calmodulin repeat homology <EFT3>;2/Modified site: acetylated amino end (Ala) (in mature ;105,262,286/Active site: Cys, His, Asn #status predicted)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S10590
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A; Residues: 1-668 <CAP>
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A;Title: Sequence of Dictyostelium DIRS-1: an apparent retrotransposon with inverted A;Reference number: A94654; MUID:86079481; PMID:2416457
A;Accession: C24785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein 668 - slime mold (Dictyostelium discoideum) transposon C:Species: Dictyostelium discoideum C:Dshate: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 18-Jun-1993 C:Accession: C24785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
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Cell 43, 10
            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene: GDB:CAPN2; mCANP; CANPml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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   Score 48.5;
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Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       calpain II catalytic chain; high-calcium
                                                  #status predicted
   DB
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                                                                                  #status
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RESULT 12 D64595

Nature

R; Tomb,

C;Date: 09-Aug-1997 #sequence_revision C;Accession: D64595

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKe son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, Wature 388, 539-547, 1997

McKe

밁 δÃ

159

KSKKMLYSEPEVLKALLEKL 178 KWKKLLKKPPPLLKKLLKKL 20 C; Superfamily:

uroporphyrinogen decarboxylase

Query Match Best Local Matches

Similarity

45.7%;

Score 48; Pred. No.

26;

2;

Conservative

Ψ

Mismatches

6; Length

Indels

0,:

Gaps

0

O

פ

uroporphyrinogen decarboxylase - Helicobacter pylori (strain 26695) C;Species: Helicobacter pylori

09-Aug-1997

#text_change

22-Jun-1999

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A; Experimental C; Genetics:
                                   A; Molecule type: DNA
A; Residues: 1-339 <ARN>
A; Cross-references: GB: AE001487;
                                                                                                                                                                                                                                  C; Species: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ripeu, J.H.; Lee, M.S.; Chen, K.T.; Chang, G.D.; Chou, C.K.; Huang, C.J.
Biochim. Biophys. Acta 1306, 133-136, 1996
A;Title: Genomic structure of carp mitogen-activated protein kinase kinase 1 gene.
A;Reference number: S70028; MUID:96221282; PMID:8634328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
S70028
                                                                                                                                                                                                                          A; Variety:
                                                                                                                                                                                                                                                    uroporphyrinogen decarboxylase -
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                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; not compared with conceptual translation A;Molecule type; DNA A;Molecule type; DNA A;Residues: 1-7;8-14;15-21;22-28;29-35;36-42;43-49;50-56;57-63;64-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mitogen-activated protein kinase kinase 1 - common carp (fragments) C;Species: Cyprinus carpio (common carp) C;Date: 14-Apr.1998 #sequence_revision 24-Apr.1998 #text_change 17-Mar.1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: S700;
R; Leu, J.H.; Lee,
                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
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hemE
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                                                                                                                                                                                                                                                                                                                                                                                         Similarity 43.07; Conservative
                                                                                                                                                                                                                                                                                                                               IVNEPPPVMKCLMKKM
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                         strain
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                              GB:AE001439; NID:g4155086; PIDN:AAD06123.1; PID:g415
                                                                                                                                                                                                                                              Helicobacter pylori (strain
                                                                                                                                                                                                                                                                                                                                                                                                       Score 48;
Pred. No.
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5; Mismatches
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H.O.; Fras ter pylori.

Fraser,

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A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: D64595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-340 <TOM>
A; Cross-references: GB; AE000574; GB; AE000511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzber, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: A81707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-dependent Clp proteinase, chain B TC0389 [imported] - Chlamydia muridar C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001 C;Accession: A81707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-867 <TET>
A;Cross-references: GB:AE002306; GB:AE002160; NID:g7190428; PIDN:AAF39246.1;
A;Experimental source: strain Nigg (MoPn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;211/Binding site: ATP (Lys) #status predicted F;611/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type:
                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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                                        A; Molecule type: mRNA
A; Residues: 1-2897 <SCH>
                                                                                                            A;Reference number: A48666; MUID:94043435; PMID:8227122 A;Accession: B48666
                                                                                                                                                                                A; Title: The cell proliferation-associated antigen of antibody Ki-67: a very
                                                                                                                                                                                                          C;Accession: B48666
C;Accession: Graces, M.; Wohlenberg, C.; Becker, M.H.G.; Key, G.; Flad, R;Schlueter, C.; Duchrow, M.; Wohlenberg, C.; Becker, M.H.G.; Key, G.; Flad, J. Cell Biol. 123, 513-522, 1993
                                                                                                                                                                                                                                                                                                                         cell proliferation antigen Ki-67, short form - human
                 A; Cross-references: EMBL: X65551
                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                            B48666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: endopeptidase Clp ATP-binding chain Keywords: ATP; molecular chaperone; nucleotide binding; 205-212/Region: nucleotide-binding motif A (P-loop) 273-278/Region: nucleotide-binding motif B 5605-612/Region: nucleotide-binding motif A (P-loop) 673-678/Region: nucleotide-binding motif B
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llarity 47.4%;
Conservative
interaction domain homology
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Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
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68;
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    Chlamydia muridarum (strain

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Search completed: Job time : 14.5 se

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A48666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
There 9; Conserv
                                                                                                                                                                                                                                                                                                                                                   C;Accession: A48666
R;Schlueter, C.; Duchrow, M.; Wohlenberg, C.; Becker, M.H.G.; Key, G.; Flad, J. Cell Biol. 123, 513-522, 1993
                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                  cell proliferation antigen Ki-67, long form - human C; Species: Homo sapiens (man)
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F; 29-91/Domain:
                                                                                                                         A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosidues: 1-3256 <SCH>
A;Cross-references: EMBL:X65550; NID:g415818; PIDN:CAA46519.1;
A;Cross-references: EMBL:X65550; NID:g415818; PIDN:CAA46519.1;
C;Superfamily: kinase interaction domain homology
C;Keywords: alternative splicing; cell cycle control; nucleus;
C;Keywords: alternative splicing; cell cycle control; nucleus;
F;29-91/Domain: kinase interaction domain homology <KIH>
                                                                                                                                                                                                                                                                                   A; Reference number: A48666; MUID: 94043435; PMID: 8227122
                                                                                                                                                                                                                                                                                                                             A;Title: The cell proliferation-associated antigen of antibody Ki-67: a very large, u
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                                                         Query Match
Best Local 9
                                       Matches
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176 KRKSLVMHTPPVLKKIIKE 194
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9; Conserva
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KWKKLLKKPPPLLKKLLKK 19
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Pred. No. 2.4e+02;
                                              Score 48; DB 2; pred. No. 2.7e+02; % Mismatches 5;
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                                                                                     Length 3256;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US06_EUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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(without alignments)
133.213 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                Length
                                       GenCore version 5.1.6 (c) 1993 - 2003 Compugen
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                                         Gapext 0.5
                                   US-10-081-418-2
US-99-876-904A-15
US-09-876-904A-629
US-09-976-904A-629
US-09-999-745-55
US-09-999-745-59
US-09-999-745-79
US-09-999-745-79
US-09-800-619-125
US-09-800-63A-49
US-09-800-053A-49
US-09-800-053A-49
US-09-800-707A-9
US-09-804-707A-9
US-09-804-707A-9
US-09-804-707A-9
US-10-051-902-20
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US-10-051-902-20
US-10-051-902-20
US-10-051-902-20
US-10-051-902-20
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US-09-804-761-40695
US-09-864-761-40695
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                                Sequence 2, Appli
Sequence 15, Appl
Sequence 629, Appl
Sequence 39, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 49, Appl
Sequence 56, Appl
Sequence 9, Appli
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 98, Appl
Sequence 98, Appl
Sequence 98, Appl
Sequence 4099, A
Sequence 40999, A
Sequence 40895, A
Sequence 40895, A
                                                                                                                                                                                                                                                                                                                          Description
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RESULT 2
US-09-876-904A-15
is Sequence 15, Application US/09876904A
publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF F
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                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: peptide with increased \cdot + ; OTHER INFORMATION: substituting amino acids US-10-081-418-2
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US-10-081-418-2
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Publication No. US20030096745A1
GEMERRAL INFORMATION:
APPLICANT: HAHM, Kyung-Soo
APPLICANT: LEE, Dong Gun
APPLICANT: PARK, YOONKYUNG
APPLICANT: ELM, Hee Nam
TITLE OF INVENTION: No. US20030096745A1el peptides with increased +
TITLE OF INVENTION: substituting one or more amino acids of CA-MA p
TITLE OF INVENTION: bharmaceutical compositions containing thereof
FILE REFERENCE: 428.1014
                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 20; Conser
                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/081,418
CURRENT FILING DATE: 202-02-22
NUMBER OF SEO ID NOS: 2
SOFTWARE: Kopatentin 1.71
SEQ ID NO 2
LENGTH: 20
TYPE: PRT
                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44
44
                                                                                                                                                                          1 KWKKLLKKPPPLLKKLLKKL
                                                                                                                                                            KWKKLLKKPPPLLKKLLKKL
                                                                                                                                                                                                                100.0%;
ilarity 100.0%;
Conservative (
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US-10-051-902-22
US-10-051-903-22
US-09-820-053A-68
) US-09-820-053A-46
) US-09-820-053A-46
) US-09-820-053A-46
) US-09-820-053A-55
10 US-09-843-845-17
10 US-09-843-845-17
10 US-09-820-053A-1218
9 US-10-061-909-28
9 US-10-060-019-29
9 US-10-060-019-29
9 US-10-060-019-29
9 US-10-060-019-29
10 US-09-954-043-4
9 US-10-954-043-4
9 US-10-954-043-4
10 US-09-820-053A-161
9 US-09-820-053A-161
9 US-09-9030-6139-2
10 US-09-9030-6139-2
10 US-09-954-898-199
10 US-09-956-888-077-1
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Pred. No. 1.7e-07;
D; Mismatches 0;
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                             PLASMID
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                          DNA (LIPOGENES TM)
                                                                                                                                                                                                                                           Length
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Sequence 22, Appl
Sequence 24, Appl
Sequence 44, Appl
Sequence 46, Appl
Sequence 48, Appl
Sequence 55, Appl
Sequence 17, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 9, Appl
Sequence 161, Appl
Sequence 172, Appl
Sequence 173, Appl
Sequence 172, Appl
Sequence 172, Appl
Sequence 172, Appl
Sequence 173, Appl
Sequence 173, Appl
Sequence 174, Appl
Sequence 175, Appl
Sequence 175, Appl
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Sequence 177, Appl
Sequence 177, Appl
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Scoring table:

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US-09-876-904A-629; Sequence 629; Application US/09876904A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC;
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEO ID NOS 629
SOFTWARE: Patentin Ver. 2.1
SEO ID NO 629
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                                                                                                                                                                     sequence 55, Application US/09999745
Patent No. US20020157120A1
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                                                                                                                                                   GENERAL INFORMATION:
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               APPLICANT: Tsien, Roger Y.
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
FILE REFERENCE: REGEN1470-1
CURRENT APPLICATION NUMBER: US/09/999,745
CURRENT FILING DATE: 2001-10-23
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                 APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Synthetic amphiphilis OTHER INFORMATION: fusogenic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICATION NUMBER:
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Pred. No. 0
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Pred. No. 0.
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; OTHER INFORMATION: Calmodulin binding peptide-2 US-09-999-745-55
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LENGTH: 17
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 39
LENGTH: 17
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Best Local
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NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                               APPLICANT: Monahan, Sean D
APPLICANT: Slattum, Paul M
APPLICANT: Slattum, Paul M
APPLICANT: Budker, Vladimir G
APPLICANT: Budker, Vladimir G
APPLICANT: Rozema, David B
TITLE OF INVENTION: INTRAVASCULAR DELIVERY OF NON-VIRAL NUCLEIC ACID
TILE REFERENCE: Mirus 013:03
CURRENT APPLICATION NUMBER: US/09/447,966
CURRENT APPLICATION NUMBER: US/09/447,966
CURRENT FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: 60/121730
PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tsien, Roger Y.
APPLICANT: Miyawaki, Atsushi
APPLICANT: Miyawaki, Atsushi
TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
TITLE OF INVENTION: DETECTION OF ANALYTES
FILE REFERENCE: 07257/042001
CURRENT APPLICATION NUMBER: US/09/554,000
CURRENT FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 08/818,252
PRIOR FILING DATE: 1997-03-14
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PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1999-07-30
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76.5%;
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                                                                                                                                                                                                                                               US-09-820-053A-49
                                                                        CURRENT APPLICATION NUMBER: US/09/820,053A
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 165
SOFTMARE: PATENTIN VET. 2.1
SEQ ID NO 49
                                                                                                                                                                                                Sequence 49, Application US/09820053A Publication No. US20030083243A1 GENERAL INFORMATION:
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LENGTH: 26
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Sequence 125, Ap
Patent No. US200
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                                                                                                                                                     FILE REFERENCE: HELX027
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SOFTWARE: FastSEQ fo
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                                                                                                                                                                   TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
                                                                                                                                                                                     APPLICANT: Owen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                        TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT: West, Michael H.P.
UPPLICANT: MCNICOL, Patricia J.
UTLE OF INVENTION: COMPOSITIONS AND
UTLE OF INVENTION: INFECTIONS USING
UTLE OF INVENTION: WITH ANTIBIOTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
OTHER INFORMATION: SYNTHETIC SEQUENCE
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                                                            ENGTH:
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                                                                                                                                                                                   Donald R.
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76.58;
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Pred. No.
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CATIONIC PEPTIDES AL
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Best Local Similarity
Matches 12; Conserv
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LENGTH: 23
TYPE: PRT
ORGANISM: ARTIFICIAL SEQUENCE
FEATURE:
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Best Local Similarity
                                                                                                                                                           SOFTWARE: PatentIn Ver. SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/10038557A Publication No. US20030092684A1
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                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/038,557A
CURRENT FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: 09/840,707
PRIOR FILING DATE: 2001-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 200
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn Ver. 2
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                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/562,979
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/198,210
PRIOR FILING DATE: 1999-04-27
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                                OTHER INFORMATION: IL-1 receptor intracellular ligand protein OTHER INFORMATION: comprising amino acid sequence PUBLICATION INFORMATION:
                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS FILE REFERENCE: 24881-301D
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Fredeking, Terry M. APPLICANT: Ignatyev, George M.
                                                                                       TYPE: PRT ORGANISM: Homo sapiens FEATURE:
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PATENT DOCUMENT NUMBER: 5,817,476
PATENT FILING DATE: 1995-06-07
                                                                                                                                            ENGTH: 700
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Pred. No. 3.9;
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Patent No. U
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Best Local
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Best Local :
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                                                      APPLICANT: ZHOU, YÜN-PING
APPLICANT: OTANI, KENICHI
APPLICANT: HANIS, CRAIG L.
APPLICANT: BELL, GRAEME I.
APPLICANT: BELL, GRAEME I.
TITLE OF INVENTION: METHODS OF TREATMENT.OF TYPE 2 DIABETES
FILE REFERENCE: ARCD:307
CURRENT APPLICATION NUMBER: US/09/768,877
CURRENT FILING DATE: 2001-01-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING HEMORRHAGIC VIRUS TITLE OF INVENTION: INFECTIONS AND OTHER DISORDERS FILE REFERENCE: 24881-301C CURRENT APPLICATION NUMBER: US/09/840,707A CURRENT FILING DATE: 2001-04-23 PRIOR APPLICATION NUMBER: 09/562,979 PRIOR APPLICATION NUMBER: 09/562,979 PRIOR FILING DATE: 2000-04-27 PRIOR PILING DATE: 2000-04-27 PRIOR FILING DATE: 1909-04-27
                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: IL-1 receptor intracellular ligand protein OTHER INFORMATION: comprising amino acid sequence PUBLICATION INFORMATION: PATENT DOCUMENT NUMBER: 5,817,476
PATENT FILING DATE: 1995-06-07
PUBLICATION DATE: 1998-10-06
   PRIOR APPLICATION NUMBER: 09/422,869
PRIOR FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 30
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SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                            APPLICANT: POLONSKY, KENNETH S. APPLICANT: HORIKAWA, YUKIO
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TYPE: PRT
ORGANISM: Homo sapiens
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Local Similarity 52.6%;
les 10; Conservative
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COX, NANCY J.
SREENAN, SEAMUS
                                                                                                                                                                                                                                                                                                                                    Application US/09768877
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Pred. No. 1
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Pred. No. 1.
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; ORGANISM: Human
US-09-768-877-23
                                         US-10-051-909-20
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LENGTH: 513
TYPE: PRT
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SOFTWARE: Microsoft O:
SEQ ID NO 20
LENGTH: 513
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Best Local :
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APPLICANT: Allen, Steve
APPLICANT: Hitz, Bill
Query Match
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/10051909 Publication No. US20020199217A1
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                                                                                                                                                           APPLICANT: Kinney, Tony
APPLICANT: Tingey, Scott
TITLE OF INVENTION: Plant Sugar Transport Proteins
FILE REFERENCE: BB1163 US CIP
CURRENT APPLICATION NUMBER: US/10/051,909
CURRENT FILING DATE: 2002-01-17
PRIOR APPLICATION NUMBER: 60/083,044
PRIOR FILING DATE: APP11 24, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tingey, Scott
TITLE OF INVENTION: Plant Sugar Transport Proteins
FILE REFERENCE: BB-1163
CURRENT APPLICATION NUMBER: US/10/051,902
CURRENT FILING DATE: 2002-01-17
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/291,922
PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-14
NUMBER OF SEQ ID NOS: 30
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                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Allen,
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                                                        ORGANISM: Zea mays
                                                                           TYPE: PRT
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Hitz, Bill
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   45.78;
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Pred. No. 1.2e
5; Mismatches
   Score 48;
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Pred. No. 1e+02;
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   Length 513;
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Best Local Similarity 43.8%; Pred. No. 1e+02;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Oy 2 WKKLLKRPPPLIKKLL 17

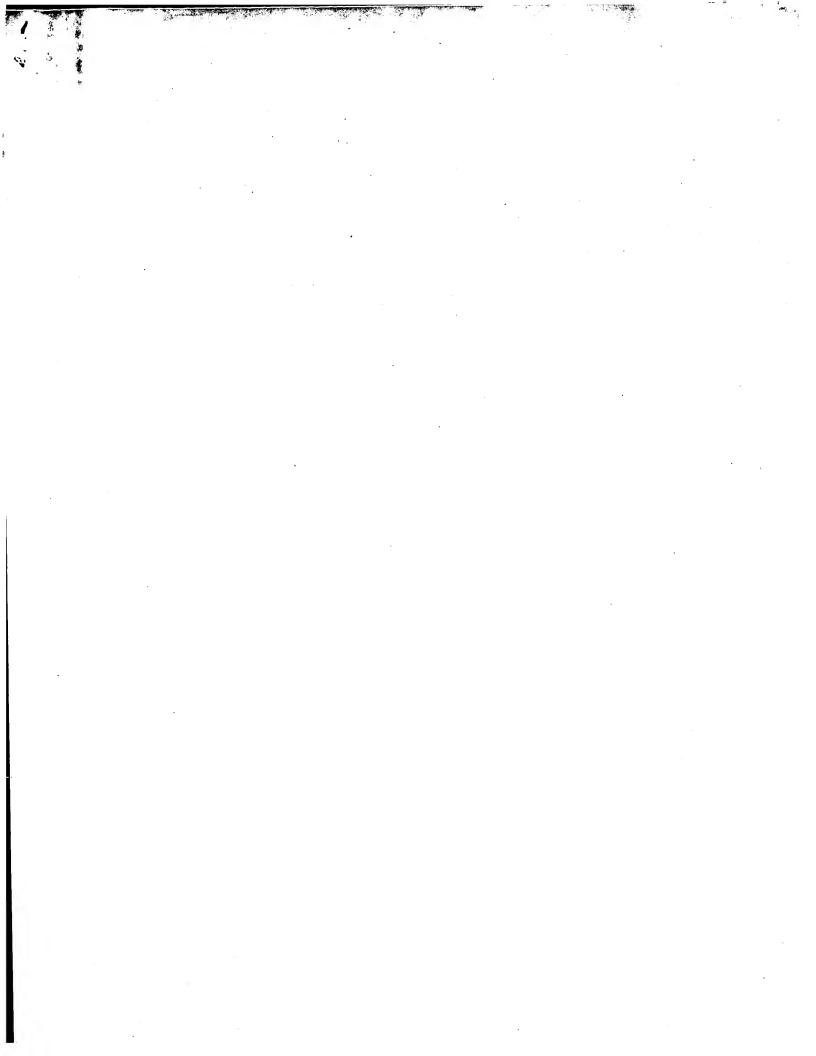
Db 267 WKKLILSTPANREL 282

RESULT 15
US-09-919-172-98
: Sequence 98, Application US/09919172
: Patent No. US20020119463A1
: GENERAL INFORMATION:
A PAPLICANT: Furner, Christopher M.
ITTLE OF INVENTION: PROSTATE CANCER MARKERS
: FILE REFERENCE: PA-0036 US
: CURRENT APPLICATION UNMERS: US/09/919,172
: PATOR APPLICATION UNMERS: US/09/919,172
: PATOR FILING DATE: 2001-07-30
: PATOR FILING DATE: 2001-07-28
: NUMER OF SEQ ID NOS: 102
: SOFTWARE: PEEL Program
: CRANNISM: Homo sapiens
: FRAURE:
: ONE INFORMATION: Incyte ID No. US20020119463A1 2700132CD1
: US-09-919-172-98
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No. US20020119463A1 2700132CD1
: US-09-919-172-98
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No. US20020119463A1 2700132CD1
: OBSTANCHES 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

MATCHES 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

SEATCH completed: June 6, 2003, 13:26:03

Search completed: June 6, 2003, 13:26:03
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Title:
Perfect score:
Sequence:
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                    protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_phage:*
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sp_bacteria:*
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1110
           5 09GRQ3
16 08YMP7
5 045769
15 09GV1
5 09GV1
16 09PN54
5 09G84
5 096849
5 09889
5 09889
6 099BB1
4 08WU26
6 09GLG1
116 09PKS5
15 09WCA9
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Oggrq3 leishmania
Ogfjp3 arabidopsis
OBxmh7 clostridium
O45769 caenorhabdi
Oglym6 arabidopsis
Oggq51 dictyosteli
Oggn54 campylobact
O4373 saccharomyc
O96849 dictyosteli
O23898 dictyosteli
O39bb1 homo sapien
O89u26 homo sapien
O99gc1 gallus gall
O29ks5 chlamydia m
O9wca9 human immun
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ALIGNMENTS

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Matches 10
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Q9FJP3;
Q1-MAR-2001
                                              Q8XMH7
Q8XMH7;
Q1-MAR-2002
Q1-MAR-2002
Q1-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Goldsmith A.D., Yiang P.X., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Naguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; Tracy S.E., Shinozaki K., Davis R.W., "Full Length cDNA of gene MQN23.16/AT5g65220 (GI:10178184)."; submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabldopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheog
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
50S ribosomal protein L29 (Putative 50S ribosomal protein
Hypothetical protein CPE0712. CPE0712. CPE0712. Clostridium perfringens. Bacteria; Firmicutes; Bacillus/Clostridium
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Pfam; PF00831; Ribosomal_L29; 1.
TIGRFAMs; TIGR00012; L29; 1.
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11 protein CPE0712.
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                                                annotation
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Karlin-Neumann
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Miranda M.,
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STRAIN=13 / TYPE A;
PubMed=11792842;
Shimian T
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Hypothetical protein;
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Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridiales; C
NCBI_TaxID=1502;
Q9LYM6;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable eukaryotic translation initiation factor 3 subunit (Putative eukaryotic translation initiation factor 3 subunit F18021_110 OR AT3G56150.
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Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caer
NCBI_TaxID-6239;
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                                                                                                                                                                                                               Q9LYM6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z93388; CAB07663.1; -.
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AP003187; BAB80418.1; -
hetical protein; Complete
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369 AA; 43506 MW;
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Pred. No.
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                                                                                                                                                                                                                                                STRAIN-AX4; TRANSPOSON-GYPSY-LIKE LTR RETROTRANSPOSON DGLT-A1; Glockner G., Szafranski K., Winckler T., Dingermann T., Quail Cox E., Eichinger L., Noegel A.A., Rosenthal A.; "The Complex Repeats of Dictyostellum discoideum."; Genome Res. 11:585-594(2001).
EMBL; AF298204; AAG37039.1; -.
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Eukaryota; Myc
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                              Pfam;
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cetozoa; Dictyosteliida;
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Carninci P., Chen H., Cheuk R.,
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YDR496C O
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Basham D., Chillingworth T., Davies R.M., Feltwell
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., I
Quail M.A., Rajandream M.A., Rutherford K.M., van
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Car
SEQUENCE FROM N.A.
Dietrich F.S., Mulligan
Carpenter J., Chen E.,
                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyc
Saccharomycetales; Saccharomycetaceae; Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL139077; CAB73497.1; --
HSSP; P06132; 1URO.
InterPro; IPR000257; Urc_decarbxyls
Pfam; PF01208; URO-D; 1.
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RNA-directed DNA polymerase.
SEQUENCE 1437 AA; 164174 MW; 7242331E6
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PROSITE; PS00907; UROD_2; UNKNOWN_1.
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Nature 403:665-668(2000).
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., Chung E.,
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                                                                                                                                                                                             MEDLINE=86079481; PubMed=2416457; Cappello J., Handelsman K., Lodish H.F.; "Sequence of Dictyostelium DRS-1: An apparent retrotransposon with inverted terminal repeats and an internal circle junction sequence.
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-85085937; PubMed-6096693;
Cohen S.M., Cappello J., Lodish H.F.;
"Transcription of Dictyostelium discoideum
                                                                  RNA-directed DNA polymerase. SEQUENCE 608 AA; 70317 MW;
                                                                                                             Pfam; PF00078; rvt;
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EMBL; M11339; AAA33195.1; -.
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Eukaryota; Mycetozoa; Dictyosteliida;
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Submitted (JUN-1997) to tl
EMBL; U33057; AAB64938.1;
SGD; S0002904; YDR496C.
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Pfam; PF00806; PUF; 4.
SMART; SM00025; Pumilio; 6.
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                                                                                                                                IPR000477;
                                                                                                                                                                                                                                                                                                                                                         Biol. 4:2332-2340(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (D.discoideum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
(D.discoideum) transposon DIRS-1, comple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    656 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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  46.2%;
47.6%;
                                                                                                                                  RVTse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; -.
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Score
Pred.
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Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                  · BE89A7F0ED84AE73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H.F.;
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No. 63;
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                                                                    CRC64;
                    Length 608;
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RESULT
Q9HBB1
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Best Local
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                                                                                                                                  "cDNA cloning by amplification of circularized first reveals non-IRE-regulated iron-responsive mRNAs."; Biochem. Biophys. Res. Commun. 275:223-227(2000). EMBL; AF261089; AAF99682.1; -. HSSP; P04574; 1ALV.
SMART; SM00230; CysPc; 1.
SMART; SM00034; EFH; 3.
PROSITE; PS00018; EF_HAND; UNKNOWN_1.
PROSITE; PS00139; THIOL_PROTEASE_CYS;
                                               Pfam; PF01067; Calpain_III; 1
Pfam; PF00036; efhand; 3.
Pfam; PF00648; Peptidase_C2;
PRINTS; PR00704; CALPAIN.
                                                                                                InterPro; IPR002048;
InterPro; IPR001300;
InterPro; IPR000169;
                                                                                                                                                                                                              TISSUE=BRAIN ASTROCYTOMA; MEDLINE=20403900; PubMed=
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                             Calpain large polypeptide L2.
                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                            Q9HBB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cappello J., Handelsman K., Lodish H.F.;
"Sequence of Dictyostellum DIRS-1: an apparent retrotransposon inverted terminal repeats and an internal circle junction seque Cell 43:105-115(1985).

EMBL; M11340; AAA70202.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 19, Last seque
01-DEC-2001 (TrEMBLrel. 19, Last annot
Hypothetical 70.4 kDa protein.
Dictyostelium discoideum (Slime mold).
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MEDLINE=86079481; PubMed=2416457;
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01-NOV-1996
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                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000477; RVTse.
Pfam; PF00078; rvt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Mycetozoa;
                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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512 QWKQCLAFPPPILLPSILEKM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 protein; RNA-directed DNA polymerase.
608 AA; 70376 MW; B7285DAB3FE2FBF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                               PubMed=10944468;
                                                                                                 SHprot_acsite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.2%;
47.6%;
                                                                                                             Protease_C2
                                                                                                                         EF-hand.
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Pred. No. 6
                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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RESULT 13
Q9GLG1
ID Q9GLG
AC Q9GLG
DT 01-MA
DT 0
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QBWU26
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Best Local
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01-UN-2002 (TremBirel. 21, Last
Hypothetical 80.0 kDa protein.
Homo sapiens (Human).
Eukaryota; Metayon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
          "Calpain isoforms in the eye of monkey.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF284441; AAG22771.1; -...
HISSP: P04574; IALV.
                                                                                                                                                                                                                                                                                         Q9GLG1;
                                                                                                                                         Cercopithecinae;
NCBI_TaxID=9541;
                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC021303; AAH21303.1; .

InterPro; IPR002048; EF-hand.
InterPro; IPR001300; Protease_C2.
InterPro; IPR001309; SHprot_acsite.
Pfam; PF01067; Calpain_III; 1.
Pfam; PF01067; Calpain_III; 1.
Pfam; PF00035; efhand; 3.
Pfam; PF00048; Peptidase_C2; 1.
                                                                                          TISSUE-RETINA;
                                                                                                                                                                                                       Macaca fascicularis
                                                                                                                                                                                                                           Calpain 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein. SEQUENCE 700 AA; 80009 MW;
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SMART; SM00230; Cyspc; 1.
PROSITE; PS00018; EF_HAND; UNKNOWN_2.
PROSITE; PS00139; THIOL_PROTEASE_CYS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (JAN
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Q8WU26;
01-MAR-2002 (TIEMBLIEL.
01-MAR-2002 (TIEMBLIEL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                         Macaca.
                                                                                                                                                                 (Crab eating macaque) (Cynomolgus monkey). Chordata; Cranlata; Vertebrata; Euteleosto Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.2%;
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                                                                                                                                                                                                                                     16,
16,
21,
                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 48.5; D
Pred. No. 72;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
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Pred. No. 72;
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 55
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                                                               Similarity
8; Conserv
WDRLKKKPPPSLPR
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Q9YGC1
Q9YGC1;
Q9YGC1;
Q9YGC1;
O1-MAY-1999 (TrEMBLrel. 10, C:
O1-MAY-1999 (TrEMBLrel. 10, L:
O1-MAR-2002 (TrEMBLrel. 20, L:
B cell linker protein BLNK.
                                                                  PRINTS; PRO1217; PRICHEXTENSN.
PRINTS; PRO0401; SH2DOMAIN.
PRODOM; PD000093; SH2; 1.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50001; SH2; 1.
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InterPro; IPR001300; Protease_C2.
InterPro; IPR001169; SHProt_acsit
Pfam; PF01067; Calpain, III; 1.
Pfam; PF00036; efhand; 3.
Pfam; PF00036; efhand; 3.
Pfam; PF00648; Peptidase_C2; 1.
PRINTS; PR00704; CALPAIN.
SMART; SM00230; CysPc; 1.
SMART; SM00054; EFh; 3.
                                                                                                                                                                                                                        "BASH, a novel signaling molecule of the bursa of Fabricius.",
J. Immunol. 161:5804-5808(1998).
EMBL; AF089727; AAD12783.1; -
EMBL; AB015289; BAA36275.1; -
HSSP; P08487; 2PLD.
                                                                                                                                                                        InterPro; IPR002965; P_rich_extensn.
InterPro; IPR000980; SH2.
Pfam; PF00017; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=99146381; PubMed=10023776;
Ishiai M., Kurosaki M., Pappu R., Okawa K.,
Ishibata M., Iwamatsu A., Chan A.C., Kurosaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; (Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                            Goitsuka R., Fujimura Y., Mamada H., U
Uetsuka K., Doi K., Tsuji S., Kitamura
                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99049801; PubMed-9834055;
                                                                                                                                                                                                                                                                                                                                                                                                                  Immunity 10:117-125(1999).
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PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.
SEQUENCE 700 AA; 80026 MW; DCEE16214F05057C CRC64;
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10; Conservative
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IPR000169; SHprot_acsite
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Last sequence update)
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5; Mismatches
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                                                                     FB232179BE38D072 CRC64;
     Mismatches
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RESULT 15
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Search completed: June Job time: 24.5 secs
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InterPro; IPR00359; AAA_ATPASe_centr.
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InterPro; IPR004176; Clp_N.
Pfam; PF00004; AAA; 1.
Pfam; PF00004; AAA; 1.
Pfam; PF00305; CLPPROTEASEA.
SMART; SM00382; AAA; 1.
PROSITE; PS00870; CLPAB_1; 1.
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EMBL; AE002306; AAF39246.1; -.
TICR; TC0389; -..
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O9PKS5;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ATP-dependent Clp protease, subunit B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia muridarum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
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Complete proteome.
SEQUENCE 867 AA; 96603 MW;
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STRAIN-MOPN / NIGG;
MEDLINE=20150255; PubMed=10684935;
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                                                                                                                           2 WKKLLKKPPPLLKKLLKKL 20
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                          6, 2003, 13:24:54
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        IF38_ARATH
Y107_NEVAC
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CAN2_HUMAN
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POLIZ_GMM
POLIZ_HOME
GAG_BAEVM
PBP4_HAEIN
CAN2_MOUSE
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049160 arabidopsis
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Q95509 fowlpox vir
Q921m8 helicobacte
P46013 homo sapien
P13026 hungarian g
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P03341 baboon endo
P45161 h penicilli
Q08529 mus musculu
Q07009 rattus norv
P14935 methanbact
P34305 caenorhabdi
Q59147 pyrococcus
P46038 frankia aln
P57964 pasteurella
P31939 homo sapien
P07834 saccharomyc
P12822 oryctolagus
P47535 mycoplasma
P56950 canis famil
P23804 mus musculu
P56951 equus cabal
Q00987 bomo sapien
Q9478 yubrio cahol
Q92178 gallus gall
P3994 schizosacch
P21190 saccharomyc
P02777 bos taurus
Q14933 homo sapien
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01-NOV-1995 (Rel. 32, Las
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01-NOV-1997 (Rel. 35, Las
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phosphorylase B kinase alpha regulatory chain.
(Phosphorylase kinase alpha L subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-C6;
MEDLINE-94303173; PubMed-8030224;
Avres M.D., Howard S.C., Kuzio J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Lagomorpha; Leporid
                                                                                                                                                         -
                                                                                                                                                                                                                                                                                                                                                                                                     Davidson J.J.,
Kilimann M.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92196064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHKA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPB2_RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RABIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=46015;
                                                                                                                                                                                                                                                                                                                                                                        "cDNA cloning of a liver isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            w
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PATHWAY: Glycogen metabolism.
SUBUNIT: POLYMER OF 16 CHAINS,
AND DELTA. ALPHA AND BETA ARE 1
CATALYTIC CHAIN, AND DELTA IS
                                                                                                                  ENZYME REGULATION: BY PHOSPHORYLATION AND BY CALCIUM.
                                                                                                                                                                                  CHAIN MAY BIND CALMODULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s M.D., Howard S.C., Kuzio J., Lopez-Ferber M., l
complete DNA sequence of Autographa californica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L22858; AAA66737.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     0ezelik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=1372435;
zelik T., Hamach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12547 MW;
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Last annotation update)
protein in HB55-PK2 intergenic region.
a nuclear polyhedrosis virus (AcMNPV).
s, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Hamacher C.,
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                                                                                                                                                                                                                                                                                                                                     of the to xp22.
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   REGULATORY
CALMODULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49;
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.2-p22.1, the region of hum.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Willems
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                                                                                                                                                         OF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus
                               CHAINS, GF
                                                                                                                                                         VARIOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
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                                                                                                                                                                                                                                                                                                                                                                                                                                 P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                  PHOSPHORYLATION IN I. THE ALPHA
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nuclear
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                                   GAMMA IS
                                                                                                                                                         SERINE
                                                                                                                                                                                                                                                                                                                                                                                                                                     Francke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND
                                                                  BETA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORF107
                                                                                                                                                         RESIDUES
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                                                                  GAMMA
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;
                                                                                                                                                                                                                                                                                                                                           human
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CAN2_HUMAN
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  P17655; Q16738;
01-AUG-1990 (Rel. 1
01-AUG-1990 (Rel. 1
15-JUN-2002 (Rel. 4
                                                                                                                                                                                                                                                                                          Imajoh S., Suzuki K.;
"The crystal structure of calcium-free human m-calpain sugges electrostatic switch mechanism for activation by calcium."; proc. Natl. Acad. Sci. U.S.A. 97:588-592(2000). reproc. catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction.
                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1990 (Rel. 15, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Calpain 2, large [catalytic] subunit precursor
(Calcium activated neutral proteinase) (CANP) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced th between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no
                                                                                   x-RAY CRYSTALLOGRAPHY (2.7 ANGSTRO)
MEDLLNE=20105516; PubMed=1063913;
Strobl S., Fernandez-Catalan C., B
Strobl S., Irie A., Sorimachi H.
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=89166474; Pi Imajoh S., Aoki K.,
                                                                                                                                                           Hata A., Ohno S., Akita Y., Suzuki K.; "Tandemly reiterated negative enhancer transcription of a human gene for the dependent protease.";
                                                                                                                                                                                                                                                         high-Ca2+-requiring form of human Biochemistry 27:8122-8128(1988).
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                     CAPN2 OR CANPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAN2_HUMAN
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                                                                         Suzuki K., Bode W.,
                                                                                                                                                                                                                      TISSUE=Lymph
                                                                                                                                                                                                                                 SEQUENCE OF 1-79
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                        MEDLINE=89197947;
                                                                                                                                                                                                                                                                      "Molecular cloning of the cDNA for high-Ca2+-requiring form of human (
                                                                                                                                                                                                                                                                                                                                                                                                                  (Millimolar-calpain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lycogen
                                                                                                                                               Biol.
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SIMILARITY: BELONGS TO THE PHOSPHORYLASE B F CHAINS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              734
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                                                                                                                                                 Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          metabolism; Phosphorylation; Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLKKPPPLLKKLLKKL
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1059 10
1235 AA;
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                                                                                                                                                 264:6404-6411(1989).
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A; 138769
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15,
41,
                                                                                                                                                                                                                                                                                                       PubMed=2852952;
., Ohno S., Emori
                                                                                                                                                                                                           PubMed=2539381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.7%;
                                                                                     Sorimachi H.,
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                                                                                                                       ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49;
Pred. No.
                                                                                                                                                                      enhancer-like for the large
                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                 Braun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B8E218C1D8C6F376 CRC64;
                                                                                                                                                                                                                                                                      Ca2+-activated
                                                                                                                                                                                                                                                                                 the
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                                                                                    Bourenkow
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20;
                                                                                                                                                                                                                                                                                 large subunit of the
                                                                                                                                                                                                                                                                                                         Kawasaki H.,
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                                                                                     Huber
kow G.,
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                                                                                                                                                                         subunit
                                                                                                                                                                                    elements
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  (M-type) (M-calpain)
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                                                  alpain suggests calcium.";
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                                                                                       Bartunik
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                                                                                                                                                                         s regulate
of calcium-
                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                         Sugihara
                                                                                     Masumoto I
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Best Local S
Matches 10
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InterPro; IPR001300; Protease_C2.
InterPro; IPR000169; SHprot_acsit
Pfam; PF00036; efhand; 3.
Pfam; PF00036; Peptidase_C2; 1.
Pfam; PF01067; Calpain_III; 1.
Pfam; PF01067; Calpain_III; 1.
PRINTS; PR00704; CALPAIN.
PRODOM; PP000012; EF-hand; 1.
SMART; SM00230; CysPc; 1.
SMART; SM00234; EFh; 2.
PROSITE; PS00018; EF_HAND; 2.
                                                                                                                    CA_BIND
CA_BIND
CA_BIND
DOMAIN
DOMAIN
ACT_SITE
ACT_SITE
                                                                                     CONFLICT
                                                                                                                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                       PROSITE; PRO0019; THIOL_PROTEASE_CYS; 1.

PROSITE; PS00639; THIOL_PROTEASE_HIS; FALSE_NEG.

PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.

PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.

Protease; Thiol protease; Calcium-binding; Repeat; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restric use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fentities requires a license agreement (See http://www.isb-sibor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M23254; AAA35645.1;
EMBL; J04700; AAA52760.1;
PIR; A31218; A31218.
PDB; 1KFU; 07-DEC-01.
                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; CO2.002; -. Genew; HGNC:1479; CAPN2.
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                                                                                                          CONFLICT
                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                             ROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (regulatory) subunit.
SUBCELLULAR LOCATION: Cytoplasmic; Translocates
membrane upon Ca++ binding.
SIMILARITY: CONTAINS 5 EF-HAND CALCIUM-BINDING [
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Met-|-Xaa Arg-|-Xaa with Leu or Val as the P2 residue.

COFACTOR: Binds 3 calcium ions.

ENZYME REGULATION: Activated by 200-1000 micromolar concentratic of calcium and inhibited by calpastatin.

SUBUNIT: Heterodiner of a large (catalytic) and a small
 213
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                                          10;
                                                     Similarity
                  KWKKLLKKPPPLLKKLLKK
EWYE-LKKPPPNLFKIIQK
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                                                                                     700
                                          Conservative
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700
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ANCESTRAL CALCIUM SITE 4 (F
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BY SIMILARITY:
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MR -> 1E (IN REF. 2):
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DOMAIN IV.
EF-HAND 1.
EF-HAND 2.
EF-HAND 3.
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CALPAIN
THIOL PR
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                                         Mismatches
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ANIN 2, LARGE [CATALYTIC] S
L PROTEASE DOMAIN I.
LIN III, C2-LIKE DOMAIN.
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RESULT 5 V226_FOWPV

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Best Local S
Matches 8
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16-OCT-2001
16-OCT-2001
15-JUN-2002
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BINDING
ACT_SITE
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16-OCT-2001
16-OCT-2001
          SEQUENCE FROM N.A.

MEDLLINE=9912057; PubMed=9923682;

Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.

Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,

Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,

Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis (
                                                                                                                                                                                                                                                                                                                                                                                         HELPJ
                                                                                                                                                                                                                                            Uroporphyrinogen HEME OR JHP0551.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prodom; PD000001; Euk_pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed; entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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J. Virol. 74:3815-3831(2000).
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Q9J509;
                                                                                                                                                                                                    Bacteria; Proteobacteria;
                                                                                                                                                                                                                     Helicobacter pylori J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                           NCBI_TaxID-85963;
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IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                            (Rel. 40, Createg)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 40,
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(Rel. 40,
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14 292 PROTEIN KINASE.
20 28 ATP (BY SIMILARITY).
43 43 ATP (BY SIMILARITY).
147 BY SIMILARITY.
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47.18;
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a; epsilon subdivision; Helicobacter group;
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4.1.1.37)
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              G.F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A. Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M. Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                               pylori.";
Nature 388:539-547(1997).
--- CATALYTIC ACTIVITY: Uroporphyrinogen-III
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Nature 397:176-180(1999)
-1- CATALYTIC ACTIVITY: Uroporphyrinogen-III - copropo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Uroporphyrinogen decarboxylase HEME OR HP0604.
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15-JUL-1998 (Rel. 36,
16-OCT-2001 (Rel. 40,
15-JUN-2002 (Rel. 41,
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HSSP; P06132; 1URO.
InterPro; IPR000257; Uro_decarbxyls
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                             Cotton M.D., Weidman J
Hayes W.S., Borodovsky
Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=26695 / ATCC 700392;
MEDLINE=97394467; PubMed=92
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SUBCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: BELONGS TO THE UROPORPHYRINGEN DECARBOXYLASE FAMILY.
                                                                                                                                   PATHWAY: Porphyrin biosynthesis.
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: BELONGS TO THE UROPORPHYRINOGEN DECARBOXYLASE FAMILY.
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InterPro; IPR000257; Uro_decu....
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                              the European Bioinformatics Institute. The use by non-profit institutions as The modified and this statement is not removed. entitles requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The cell proliferation-associated antigen of antibody Ki-67: a large, ubiquitous nuclear protein with numerous repeated element
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SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
DEVELOPMENTAL STAGE: EXPRESSION OF THIS ANTIGEN OCCURS
PREFERENTIALLY DURING LATE G1, S, G2, AND M PHASES OF THE (CYCLE, WHILE IN CELLS IN G0 PHASE THE ANTIGEN CANNOT BE DETERMENT.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: THOUGHT PROLIFERATION.
                                                          SWISS-PROT entry is copyright. It is produced and the EMBL outserent the Swiss Institute of Bioinformatics and the EMBL outserent the Swiss Institute. There are no restrictions as its content is in a sit of the swiss and for content is in the swiss and the swiss are the swiss and the swiss are the swiss are the swiss and the swiss are t
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EMBL; X94762; CAA64388.1; -.
Genew; HGNC:7107; MKI67.
MIN; 176741; -.
InterPro; IPR000253; FHA_domain.
Pfan; PF00498; FHA; 1.
SMART; SM00240; FHA; 1.
PROSITE; PS50006; FHA_DOMAIN; 1.
Cell cycle; Antigen; Nuclear prote
                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 814-822.

BEDLINE-90016865; PubMed-2798129;

Brault V., Hibrand L., Candresse T., le Gall O., Dunez J.

"Nucleotide sequence and genetic organization of Hungaria chrome mosaic nepovirus RNA2.";

Nucleic Acids Res. 17:7809-7823(1989).

-I- FUNCTION: THE PROTEIN LOCATED AT THE N-TERMINAL END COMPONITUS POLYPROTEIN COULD BE REQUIRED FOR NEMATODE OF THE VIRUS.
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                                                                                  PTM: THE RNA2 POLYPROTEIN IS CLEAVED BY AN RNA1-ENCODED PROTE
TO YIELD THE MATURE COAT PROTEIN AND AN 84 kDa PROTEIN WHICH
FURTHER CLEAVED INTO TWO PRODUCTS OF APPROXIMATELY 46 AND 48
SIMILARITY: TO THE RNA2 POLYPROTEIN OF OTHER NEPOVIRUSES.
 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EWBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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27 76 FHA.
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Matches
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Mitogen-activated protein kinase 14A (EC 2.7.1.-) (MI (D38 MAPK) (D938) (D-p38a).

(D38 MAPK) (D938) (D-p38a).

MPK2 OR P38A OR CG5475.

Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrusi Eukaryota; Metazoa; Arthropoda; Mondibulata; Diptera, Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBL_TaxID-7227;
STRAIN-Berkeley;

MEDLINE-20196006; PubMed-10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Sutton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.
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"A conserved p38 mitogen-activated p
Drosophila immunity gene expression.
Mol. Cell. Biol. 18:3527-3539(1998).
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PIR; S
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                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98079070;
                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Hemocyte;
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MEDLINE-98252940;
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Diptera; Brach
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tle R.F.,
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Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn I Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn I Durbin K.J., Evangelista C.C., Ferrac C., Ferraca S., Fleischmann I Roster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Gunar P., Harris M.A. Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeywam C., Jalai D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C., Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.J. A., Aktimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., A. Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., A. Liasko P., Lei Y., McIntosh T.C., McLeod M.P., McPherson D., A., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ra Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G. Ra Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Ra Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., Ra Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., Ra Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Shen B., Woodage T., Worley K.C., Mu D., Yang S., Yao Q.A., Ra Williams S.M., Woodage T., Worley K.C., Mu D., Yang S., Yao Q.A., Ra Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Lin Y., Ling S., Wang S., W
                                    HSSP; Q16539; INFC:
Flybase; FBgnQ015765; Mpk2.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR003527; MAP_kin.
InterPro; IPR003527; MAP_kin.
InterPro; IPR002390; Ser_thr_pkinase.
Pfam; PFQ0069; pkinase; 1.
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Ballew R.M.
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Proc. Natl. Acad. Sci. U.S.A. 89:6295-6299(1992).

-i- FUNCTION: Kinase involved in a signal transduction down regulate insect immunity gene expression after
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MEDLINE=92335284; PubM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 38-188 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYT-186 in response to environmental SUBCELLULAR LOCATION: Nuclear.
DEVELOPMENTAL STAGE: Expressed both nuevels are highest at the preblastode present throughout development.
SIMILARITY: BELONGS TO THE SER/THR FA
                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics the Eu-
European Bioinformatics Institute. There are no restr
by non-profit institutions as long as its content
                                                                                                                                                                                              AF035546; AAC39030.1; -. AF035547; AAC39031.1; -. U86867; AAB97138.1; -. AE003746; AAF56244.1; -.
                                                                                                                                                                                                                                                                                                                           non-profit institutions as long as its content is in no way d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KINASE SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
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but low levels are
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Smith H.O.,
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RESULT 11
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Best Local
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PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAG_BAEVM STANDARD; PRT; 537 AA P03341; P10268; 21-JUL-1986 (Rel. 01, Created) 01-MAR-1989 (Rel. 10, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat GAG polyprotein (Contains: Inner coat protecare shell protein P30; Nucleoprotein P10].
                                                                                                                                                                                              POLYPROTEIN.
-!- SIMILARITY: CONTAINS 1 CCHC-TYPE ZINC FINGER.
-!- CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN EXTENSIVELY.
                                                                                                                                                                                                                                                             gag-pol region.";
J. Virol. 47:137-145(1983).
-i- ptm: SPECIFIC ENNYMATIC CLEAVAGES IN VIVO YIELD
-i- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kato S., Matsuo K., Nishimura N., Takahashi N., Takano T.; "The entire nucleotide sequence of baboon endogenous virus chimeric genome structure of murine type C and simian type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT
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Nuclear prote
                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                            modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                        retroviruses."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baboon endogenous virus (strain M7).
Viruses; Retroid viruses; Retroviridae; Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                             "Provirus of M7
                                                                                                                                                                                                                                                                                                                                                               Tamura T.;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=83241915;
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D10032;
X05470;
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10; Conserv
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PS00107;
PS50011;
PS500108;
                                                       s requires a license agreement (See http://www.isb-sib.ch/announce, an email to license@isb-sib.ch).
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BAA00923.1;
CAA29027.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                      62:127-137(1987).
                                                                                                                                                                                                                                                                                                                                           baboon endogenous virus: nucleotide
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PROTEIN_KINASE_ST; F
                                                                                                                                                                                                                                                                                                                                                                                   PubMed=6408267
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PHOSPHORYLATION.
D -> G (IN REF. 2
K -> R (IN REF. 2
D -> A (IN REF. 2
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> R (IN REF. 4).
> A (IN REF. 2).
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n kinase; ATP-binding;
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. 16;
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                                                                                            Usage
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                                                                                                                   its content
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                                                                                                in no way commercial
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Best Local
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Pfam; PF01140; Gag_MA; 1.
Pfam; PF02193; Gag_P30; 1.
SMART; SM00343; ZnF_C2HC; 1.
PROSITE; PS50158; ZF-CCHC; 1.
Core protein; Coat protein; Nuc
                                                                                                                                                                                           STRAIN-Rd / KW20 / ATCC 51907;

#EDLIND=9535630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weldman J.F., Phillips C.A., Spriggs T., Hedblome E., Cotton M.D.,

Piterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Penicillin-binding protein 4 precursor (PBP-4) [Includes: D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4) (DD-peptidase) (DD-carboxypeptidase); D-alanyl-D-alanine-endopeptidase (EC 3.4.99.-) (DD-carboxypeptidase); D-alanyl-D-alanine-endopeptidase (EC 3.4.99.-) (DD-carboxypeptidase);
                      This
                                                                                                                                         Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PBP4_HAEIN
P45161;
                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
ZN_FING
LIPID
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAEIN
                                                                                                                                                                    Whole-genome xandom sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                Haemophilus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                    CATALYTIC ACTIVITY: D-alanyl-D-alanine + H(2)0 = PATHWAY: FINAL STAGES IN PRETIDOGLYCAN SYNTHESIS. SUBCELLULAR LOCATION: PERIPLISMIC (Potential). SIMILARITY: BELONGS TO PEPTIDASE FAMILY S13; ALSO D-ALANYL-D-ALANINE CARBOXYPEPTIDASE 3 FAMILY.
                                                                                                         FUNCTION: NOT INVOLVED IN TRANSPEPTIDATION BUT EXCLUSIVELY CATALYSES A DD-CARBOXYPEPTIDASE AND DD-ENDOPEPTIDASE REACT (BY SIMILARITY).
SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A03939; I
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IPR003036; Gag_P30.
IPR001878; Znf_CCHC
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                                                                                                                                                                                                                                                                                                                                                                                       gamma subdivision; Pasteurellaceae,
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Pred. No.
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CORE SHELL PROTEIN P30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                     ALSO KNOWN
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                                                                                          D-alanine
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RESULT 13
CAN2_MOSE
ID CAN2_MOSE
ID CONS_MOSE
O08529
DT 01-NOV
DT 16-OCT
DT 15-JUN
DE Calpai
DE (Calcai
DE (Milli
GN CAPN2.
OS MUS mu
OC Eukary
OC Mammal
OX NCBL_T
RN [1]
RP SEQUEN
RC STRAIN
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RL Genomi
RL SUBmit
RN [2]
RP SEQUEN
RC STRAIN
RA DESTRAIN
RA DESTRAIN
RA DESTRAIN
RA SEQUEN
RC STRAIN
RA SIASS
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RN [3]
RP SEQUEN
RC TISSUE
RA Glass
RT SUBmit
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"Cloning of m-calpain from mouse nervous system.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ dattabases.
-I- FUNCTION: Calcium-regulated non-lysosomal thiol-protease of the cattalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction (By simil:
-I- CATALYTIC ACTIVITY: Preferential cleavage: Tyr-1-Xaa, Met.
-I- COFACTOR: BIAGS 3 calcium ions.
-I- ENZYME REGULATION: Activated by 200-1000 micromolar conceled of calcium and inhibited by calpastatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CANZ_MOUSE STANDARD; PRT; 700 AA.

008529; 035518; 054843;
01-NOV-1997 (Rel. 35, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Calpain 2, large [catalytic] subunit precursor (EC 3.4.22.17)
(Calcium-activated neutral proteinase) (CANP) (M-type) (M-calpain)
(Millimolar-calpain) (80 KDa M-calpain subunit) (CALP80).
                                                                                                                                                                                                                                                                                                                                    Dear N., Matena K., Vingron M., Boehm T.;
"A new subfamily of vertebrate calpains lack
domain: implications for calpain regulation
Genomics 45:175-184(1997).
                                                                                                                                                                                                  TISSUE-CNS;
                                                                                                                                                                                                                                                     Submitted (OCT-1997)
                                                                                                                                                                                                                                                                         Ozaki Y
                                                                                                                                                                                                                                                                                      STRAIN-BALB/c;
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97480729; PubMed-9339374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00922; PRINTS; PR00922; PRINTS; PR00922; PR00666; PBP4; 1.
TIGRFAMS; TIGR00666; PBP4; 1.
TIGRFAMS; TIGR00666; PBP4; 1.
TIGRFAMS; TIGR009666; PBP4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                            EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
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Pfam; PF02113; Peptidase_S13; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR; HI1330; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U32812; AAC22975.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 KHLSKPLPDLLKKMMKK 309
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479
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1 26
07ENTIAL.
27 479
69 69 ACYLATED B
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52685
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                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45.5;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PENICILLIN-BINDING PROTEIN 4.

ACYLATED BY PENICILLIN (FORMS PART OF THE ACTIVE-SITE CLEFT) (BY SIMILARITY).

SUBSTRATE-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                632868С61206СВ48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murinae;
                     concentrations
                                                                                      similarity).
                                                                       Met-|-Xaa
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RESULT
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DT 11
DT 11
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between
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CAN2_RAT

Q07009;

01-JUN-1994

01-JUN-1994

15-JUN-2002

Calpain 2, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
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ACT_SITE
CONFLICT
CONFLICT
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DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TS; FANCE OF THE SMALL SUBUNIT (POT PROTEASE; CALPAIN 2, LARGE COMAIN I.

RT; SMO0230; CysPc; 1.

ART; SM000230; CysPc; 1.

ART; SM000230; EFFH; 2.

ROSITE; PS00018; EFFHAND; 2.

ROSITE; PS00019; THIOL_PROTEASE_HIS; FALSE_NEG.

PROSITE; PS00640; THIOL_PROTEASE_HIS; FALSE_NEG.

PROSITE; PS00640; THIOL_PROTEASE; Calcium—binding; Repeat; Multigene ANCHORS TO THE SMALL SUBUNIT (POT CALPAIN 2, LARGE [CATALYTIC] SUB-

CALPAIN 2, LARGE [CATALYTIC] SUB-

THE DOMAIN II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
DOMAIN
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InterPro; IPR002048; E
InterPro; IPR001300; P
InterPro; IPR000169; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
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Pfam; PF01067; Calpain_III; 1.
PRINTS; PR00704; CALPAIN.
ProDom; PD000012; EF-hand; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
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                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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(regulatory) subunit.
SUBCELLULAR LOCATION: Cytoplasmic; Translocates
SUBCELLULAR LOCATION: Cytoplasmic; Translocates
SUBCELLULAR LOCATION: SEF-HAND CALCIUM-BINDING
TOTAL REPUBLIC CONTAINS SEF-HAND CALCIUM-BINDING
TOTAL REPUBLIC CO.
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9; Conserv
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2 (Rel. 41, Last annotation updatalytic] subunit precur
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llarity 47.48;
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A -> G (IN REF. 2).
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UBUNIT (POTENTIAL).
LYTIC] SUBUNIT.
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kattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBT mastr-10716
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the role of the C(2)-like domain.";
J. Biol. Chem. 276:7404-7407(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deluca C.I., Davies P.L., Samis of "Molecular cloning and bacterial II 80 kDa subunit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95361909; PubMed-7635186; Arthur J.S., Gauthier S., Elce J.S.; "Active site residues in m-calpain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-95361909; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21240297;
Moldoveanu T., Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-94032492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Calcium-activated neutral proteinase) (CANP) (M-type) (M-calpain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ca(2+)-dependent protease activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20069318;
Hosfield C.M., Eld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutagenesis
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Hosfield C.M., Moldoveanu T.,
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partial proteolysis.";
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                                                                                                                                                                                                                                                                                                     This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
MEDLINE=20069318; PubMed=10601010;
                                                                                                                                                                        modified and this statement is not removentities requires a license agreement (Son send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                          esn
                                                                                                                             EMBL; L09120; AAA16327.1;
                                                                                                                                                                      or send an
                                                                                                                                                                                                                                                                                   between
                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Calcium-regulated non-lysosomal thiol-protease catalyze limited proteolysis of substrates involved in cytoskeletal remodelling and signal tranduction. CATALYTIC ACTIVITY: Preferential cleavage: Tyr-|-Xaa, Met Arg-|-Xaa with Leu or Val as the P2 residue.

COFACTOR: Binds 3 calcium ions.

ENZYME REGULATION: Activated by 200-1000 micromolar concessions.
                                                                                                                                                                                                                                                                                                                                            (regulatory) subunit.
SUBCELLULAR LOCATION: Cytoplasmic; Translocates to the membrane upon Ca++ binding.
SIMILARITY: CONTAINS 5 EF-HAND CALCIUM-BINDING DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C2.
                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                     of calcium and inhibited by calpastatin. SUBUNIT: Heterodimer of a large (catalytic) and
                                                                                 S38361; S38361.
1DF0; 21-JUN-00
                                                                  C02.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18:6880-6889(1999)
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                    IPR002048;
IPR001300;
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es P.L., Samis J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-230; LYS-234 AN PubMed=11102442;
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  FF-hand.
Protease_C2.
SHprot_acsite.
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                                                                                                                                                                                                   is not removed. Usage by agreement (See http://www.:
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Sciurognathi; Muridae;
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PRINTS; PR00704; CALPAIN. ProDom; PD000012; EF-hand; 1. Pfam; PF00036; efhand; 3. Pfam; PF00648; Peptidase_C2; 1. Pfam; PF01067; Calpain_III; 1.

SMART; SM00230; CysPc; 1. SMART; SM00054; EFh; 2.

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Best Local
                                                                                                                 MEDLINE-90221821; PubMed-2326168;
Bokranz M., Klein A., Meile L.;
"Complete nucleotide sequence of plasmid pME2001 of Methanobacterium
thermoautotrophicum (Marburg).";
Nucleic Acids Res. 18:363-363(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P14935;
01-APR-1990
01-APR-1990
15-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Hypothetical 16.7 kDa protein.
Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
Plasmid pHE2001.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
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PROSITE; PS00018; EF_HAND; 2.

PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.

PROSITE; PS00639; THIOL_PROTEASE_HIS; FALSE_NEG.
PROSITE; PS00640; THIOL_PROTEASE_ASN; FALSE_NEG.
PROSITE; PS00640; TRIOL_PROTEASE_ASN; FALSE_NEG.
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LINKER.
DOMAIN IV.
EF-HAND 1.
EF-HAND 2.
EF-HAND 3.
ANCESTRAL CALCIUM SITE 4
ANCESTRAL CALCIUM SITE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6;
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Pred. No. 36;
6; Mismatches
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CALPAIN 2, LARGE [CATALYT
THIOL PROTEASE DOMAIN II.
THIOL PROTEASE DOMAIN II.
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LOSS OF ACTIVITY.
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DECREASE OF 10% OF THE
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DECREASE OF 12% OF
NO EFFECT.
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2, LARGE [CATALYTIC] SUBUNIT.
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